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85030

From: Sullivan, Daniel  
Sent: Thursday, January 23, 2003 12:39 PM  
To: STIC-Biotech/ChemLib  
Subject: SEQUENCE SEARCH FOR 09852424

Please search for a polypeptide comprising the sequence set forth as SEQ ID NO:1-5 in the commercial and issued patent databases.

Thank you.  
Dan

Daniel M. Sullivan  
Examiner AU 1636  
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Tel: 703-305-4448

RECEIVED

JAN 23 2003

STIC/BIOTECH DIVISION  
(STIC)

Edward Hart  
Technical Info. Specialist  
STIC/Biotech  
CMI 6B02 Tel: 305-9203

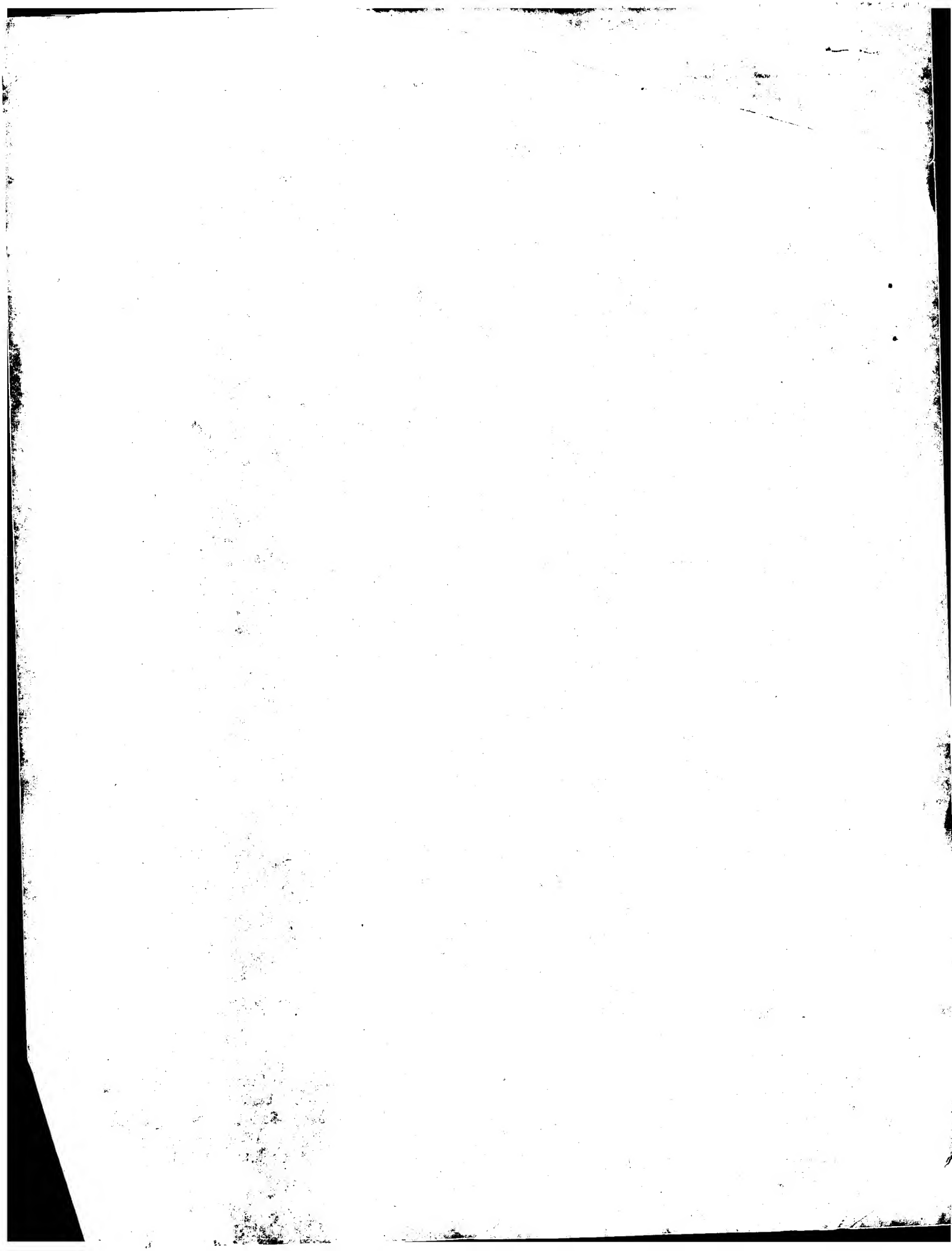
Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 1/23/03  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_  
AA Sequences: 5  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: 02  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 23, 2003, 15:27:48 ; Search time 28.2 seconds  
(without alignments)  
316.588 Million cell updates/sec

Title: US-09-852-424-1

Perfect score: 359  
Sequence: 1 KGVSLSYRCPCHRFESHVAR.....QVCIDPKLKIQVLEYLAKLN 67

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
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22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	359	100.0	67	23	AA48656
2	354	98.6	67	23	AA48658
3	354	98.1	67	23	AA48657
4	352	98.1	67	23	AA48660
5	351	97.8	67	19	AAW50760
6	351	97.8	67	20	AAV34092
7	351	97.8	67	20	AAV06741
8	351	97.8	67	20	AAV06726
9	351	97.8	67	20	AAV67594
10	351	97.8	67	23	AA847660

11	351	97.8	68	19	AAW50761	Peptide which bind
12	351	97.8	69	20	AAV05818	N-terminal modifie
13	351	97.8	72	19	AAW50762	Peptide which bind
14	351	97.8	72	20	AAV34092	Native stromal cel
15	351	97.8	73	21	AAV67595	SDF-1beta peptide
16	351	97.8	73	19	AAW50763	Peptide which bind
17	351	97.8	73	20	AAV05819	N-terminal modifie
18	351	97.8	74	21	AAV69041	Amino acid sequenc
19	351	97.8	89	16	AAV75419	Human SDF-1-alpha.
20	351	97.8	89	20	AAV39995	Human SDF-1-deriv
21	351	97.8	89	20	AAV26177	Human chemokine SD
22	351	97.8	89	21	AAV15791	A human B-cell set
23	351	97.8	89	21	AAV93603	N-terminal modifie
24	351	97.8	89	21	AAV52508	Human SDF-1-deriv
25	351	97.8	90	21	AAV05820	Human SDF-1-deriv
26	351	97.8	93	16	AAV75420	Human SDF-1-deriv
27	351	97.8	93	19	AAV50766	Human SDF-1-deriv
28	351	97.8	93	20	AAV26178	Human SDF-1-deriv
29	351	97.8	93	20	AAV06725	Human SDF-1-deriv
30	351	97.8	93	21	AAV15812	Human SDF-1-deriv
31	351	97.8	93	23	AAE23952	Human SDF-1-deriv
32	351	97.8	93	23	AAU84305	Human SDF-1-deriv
33	351	97.8	93	23	AAV47690	Human SDF-1-deriv
34	351	97.8	93	23	AAV05821	Human SDF-1-deriv
35	351	97.8	94	20	AAV05821	Human SDF-1-deriv
36	351	97.8	101	23	AAV48051	Human SDF-1-deriv
37	351	97.8	119	23	AAV48047	Human SDF-1-deriv
38	351	97.8	166	20	AAV29899	Human SDF-1-deriv
39	351	97.8	177	20	AAV29896	Human SDF-1-deriv
40	351	97.8	320	21	AAV69055	Human SDF-1-deriv
41	351	97.8	322	21	AAV69056	Human SDF-1-deriv
42	351	97.8	326	19	AAV76221	Human SDF-1-deriv
43	351	97.8	327	21	AAV9057	Human SDF-1-deriv
44	351	97.8	328	19	AAV6220	Human SDF-1-deriv
45	351	97.8	339	20	AAV29905	Human SDF-1-deriv

#### ALIGNMENTS

RESULT 1	AA48656	standard; peptide: 67 AA.
XX	AA48656;	
AC	20-MAY-2002 (first entry)	
DT	XX	
XX	XX	
DE	XX	XXCR4 peptide antagonist SEQ ID NO 1.
XX	XX	XXCR4; haematopoietic cell; chemokine receptor-4; cytosolic;
KW	XX	Immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
KW	XX	cell multiplication.
XX	XX	
OS	XX	Synthetic.
XX	XX	
PN	XX	WO200185196-A2.
PD	XX	15-NOV-2001.
XX	XX	
PF	XX	09-MAY-2001; 2001WO-CA00659.
XX	XX	
PR	XX	09-MAY-2000; 2000CA-2305787.
XX	XX	19-MAY-2000; 2000US-205467P.
XX	XX	
PA	XX	(UYBR-) UNIV BRITISH COLUMBIA.
XX	XX	(CHEM-) CHEMOKINE THERAPEUTICS CORP.
PI	XX	Tudán CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
XX	XX	Clark-Lewis I, Salari H;
DR	XX	WPI, 2002-106073/14.

PT Promoting the rate of haematopoietic cell multiplication for treating a  
 PT cancer involves administering chemokine receptor antagonist to the  
 PT cells  
 XX  
 PS Claim 9; Page 54; 68pp; English.

CC The invention relates to a method of promoting the rate of haematopoietic  
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)  
 CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist  
 CC has cytostatic and immunosuppressive activity and is useful for treating  
 CC cancer or autoimmune disease in a patient; to promote the rate of  
 CC haematopoietic cell multiplication; to formulate a medicament for  
 CC increasing the circulation of the haematopoietic cells in a patient; for  
 CC mobilising haematopoietic cells from a narrow locus to a peripheral blood  
 CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The  
 CC CXCR4 antagonists stimulates haematopoietic cell multiplication,  
 CC self-renewal, expansion and proliferation of peripheralisation in vivo.  
 CC  
 SQ Sequence 67 AA:

Query Match 100.0%; Score 359; DB 23; Length 67;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-39;  
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KGVSLSYRCPCRFESHVARANVYKHLKILNTPNCALQIVARLKNNNRQVCIDPKLWIOE 60  
 DB 1 KGVSLSYRCPCRFESHVARANVYKHLKILNTPNCALQIVARLKNNNRQVCIDPKLWIOE 60  
 OY 61 YLEKALN 67  
 DB 61 YLEKALN 67

## RESULT 2

AAM48658  
 ID AAM48658 standard; peptide; 67 AA.

AC AAM48658;

DT 20-MAY-2002 (first entry)

DE CXCR4 peptide antagonist SEQ ID NO 3.

KW CRCX4; haematopoietic cell; chemokine receptor-4; cytostatic;  
 KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;  
 KW cell multiplication.

OS Synthetic.

Key Location/Qualifiers  
 Modified-site 6

/note= "Optionally the proline analogue 6-amino-7-oxo-2,  
 3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic  
 acid residue or a bicyclic turned dipeptide  
 (Btd)"

WO200185196-A2.

15-NOV-2001.

09-MAY-2001; 2001WO-CA00659.

09-MAY-2000; 2000CA-2305787.

19-MAY-2000; 2000US-205467P.

(UYBR-) UNIV BRITISH COLUMBIA.  
 (CHEM-) CHEMOKINE THERAPEUTICS CORP.

Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;  
 Clark-Lewis I, Salari H;

WPI; 2002-106073/14.

PT Promoting the rate of haematopoietic cell multiplication for treating a  
 PT cancer involves administering chemokine receptor antagonist to the  
 PT cells  
 XX  
 PS Claim 9; Page 54; 68pp; English.

CC The invention relates to a method of promoting the rate of haematopoietic  
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)  
 CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist  
 CC has cytostatic and immunosuppressive activity and is useful for treating  
 CC cancer or autoimmune disease in a patient; to promote the rate of  
 CC haematopoietic cell multiplication; to formulate a medicament for  
 CC increasing the circulation of the haematopoietic cells in a patient; for  
 CC mobilising haematopoietic cells from a narrow locus to a peripheral blood  
 CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The  
 CC CXCR4 antagonists stimulates haematopoietic cell multiplication,  
 CC self-renewal, expansion and proliferation of peripheralisation in vivo.  
 CC  
 SQ Sequence 67 AA:

Query Match 98.6%; Score 354; DB 23; Length 67;  
 Best Local Similarity 98.5%; Pred. No. 5.5e-39;  
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KGVSLSYRCPCRFESHVARANVYKHLKILNTPNCALQIVARLKNNNRQVCIDPKLWIOE 60  
 DB 1 KGVSLPYRCPCRFESHVARANVYKHLKILNTPNCALQIVARLKNNNRQVCIDPKLWIOE 60  
 OY 61 YLEKALN 67  
 DB 61 YLEKALN 67

## RESULT 3

AAM48657  
 ID AAM48657 standard; peptide; 67 AA.

AC AAM48657;

DT 20-MAY-2002 (first entry)

DE CXCR4 peptide antagonist SEQ ID NO 2.

KW CRCX4; haematopoietic cell; chemokine receptor-4; cytostatic;  
 KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;  
 KW cell multiplication.

OS Synthetic.

Key Location/Qualifiers  
 Modified-site 5

/note= "Optionally the proline analogue 6-amino-7-oxo-2,  
 3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic  
 acid residue or a bicyclic turned dipeptide  
 (Btd)"

WO200185196-A2.

15-NOV-2001.

09-MAY-2001; 2001WO-CA00659.

09-MAY-2000; 2000CA-2305787.

19-MAY-2000; 2000US-205467P.

(UYBR-) UNIV BRITISH COLUMBIA.  
 (CHEM-) CHEMOKINE THERAPEUTICS CORP.

Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;  
 Clark-Lewis I, Salari H;

WPI; 2002-106073/14.





CC associated opportunistic infections and/or other CXCR4 or CC chemokines,  
 CC especially RANTES, MIP1- alpha , MIP1- beta or MCP1. The peptide can be  
 CC used to detect anti-SDF-1 antibodies in biological fluids. This  
 CC sequence represents a specifically claimed peptide which binds to the  
 CC CXCR4 receptor.

XX  
 SO Sequence 67 AA:

Query Match 97.8%; Score 351; DB 19; Length 67;  
 Best Local Similarity 98.5%; Pred. No. 1.4e-38;  
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KGVSLSYRCPCRFESHVARANVHKILINPNCALQIVARLKNNNROYCIDPKLKWIOE 60  
 DB 1 KPVSLSYRCPCRFESHVARANVHKILINPNCALQIVARLKNNNROYCIDPKLKWIOE 60

OY 61 YLEKALN 67  
 DB 61 YLEKALN 67

RESULT 6  
 AAY34092  
 ID AAY34092 standard; protein: 67 AA.

XX  
 AC AAY34092;  
 XX  
 DT 29-NOV-1999 (first entry)

XX Native stromal cell derived factor 1 (SDF-1) alpha protein.

XX CXCR4 chemokine receptor 4; CXCR4; antagonist; medicament; T-cell;  
 KM interferon gamma; autoimmune disease; multiple sclerosis; cancer;  
 KM angiogenesis; stromal cell derived factor 1; SDF-1.

XX Mammalia.

XX WO9947158-A2.

XX 23-SEP-1999.

XX 12-MAR-1999; 99WO-CA00221.

XX 13-MAR-1998; 98CA-2226391.

XX 14-AUG-1998; 98CA-2245224.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Clark-Lewis I, Gong J, Duronio V;

XX WPI; 1999-561857/47.

XX Use of CXCR4 chemokine receptor 4 for treating autoimmune disease and

XX cancer -

XX Example 1; Fig 1; 71pp: English.

XX The invention relates to the use of a CXCR4 chemokine receptor 4 (CXCR4)  
 CC antagonist for the manufacture of a medicament for reducing interferon  
 CC gamma production by T-cells in a mammal. The CXCR4 antagonist can be used  
 CC to treat or to design a medicament to treat, an autoimmune disease,  
 CC multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4  
 CC antagonists may be peptide compounds comprising a substantially purified  
 CC peptide fragment, analogue or a pharmacologically acceptable salt of  
 CC stromal cell derived factor 1 (SDF-1). The present sequence represents  
 CC the amino acid sequence of SDF-1 alpha protein.

XX  
 SO Sequence 67 AA:

Query Match 97.8%; Score 351; DB 20; Length 67;  
 Best Local Similarity 98.5%; Pred. No. 1.4e-38;  
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KGVSLSYRCPCRFESHVARANVHKILINPNCALQIVARLKNNNROYCIDPKLKWIOE 60  
 DB 1 KPVSLSYRCPCRFESHVARANVHKILINPNCALQIVARLKNNNROYCIDPKLKWIOE 60

OY 61 YLEKALN 67  
 DB 61 YLEKALN 67

RESULT 7  
 AAY06741  
 ID AAY06741 standard; protein: 67 AA.

XX  
 AC AAY06741;

XX 18-JUN-1999 (first entry)

XX SDF-1 alpha/RANTES cross-over chemokine control molecule SSSS.

XX Chemokine; cross-over protein; pharmaceutical; inflammatory; AIDS; viral;  
 KM infectious disease; hematopoiesis; chemoprotection; asthma; RANTES; VMP;  
 KM allergic rhinitis; atopic dermatitis; rheumatoid arthritis; SDF-1; MPV;  
 KM stromal cell derived factor 1; Macrophage inflammatory protein.

XX Synthetic.

XX Homo sapiens.

XX WO9911655-A1.

XX 11-MAR-1999.

XX 31-AUG-1998; 98WO-US18096.

XX 04-SEP-1997; 97US-0057620.

XX (GRYP-) GRYPHON SCT.

XX Kent SBH, Slani MA, Simon R, Wilken J;

XX WPI; 1999-205128/17.

XX New cross-over proteins for treatment of inflammation and infections  
 PT e.g. AIDS - prepared by ligation of two functional protein modules  
 PT derived from two different parent molecules

XX Example 4; Page 43; 75pp: English.

XX The invention relates to a cross-over protein produced by chemical  
 CC ligation of at least two functional protein modules derived from at  
 CC least two parent protein molecules. The cross-over proteins can be used  
 CC in pharmaceutical compositions for therapy of inflammatory and  
 CC infectious diseases including AIDS, and for indications of hematopoiesis  
 CC and chemoprotection. They are also useful for treatment of asthma,  
 CC allergic rhinitis, atopic dermatitis and rheumatoid arthritis. A library  
 CC comprising a collection of cross-over proteins is useful for screening  
 CC for cross-over proteins that are receptor ligands. The libraries  
 CC comprise functionally diverse compounds and libraries are exemplified by the  
 CC discovery process. The proteins and libraries are exemplified by the  
 CC preparation of cross-over chemokines comprising various combinations of  
 CC peptide segments derived from RANTES, SDF-1 (stromal cell derived factor  
 CC 1), VMP (viral Macrophage inflammatory protein) and other such  
 CC chemokines. Sequences AAY06741-62 represent amino acid sequences of SDF-1  
 CC alpha/RANTES cross-over molecules.

XX  
 SO Sequence 67 AA:

Query Match 97.8%; Score 351; DB 20; Length 67;  
 Best Local Similarity 98.5%; Pred. No. 1.4e-38;  
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KGVSLSYRCPCRFESHVARANVHKILINPNCALQIVARLKNNNROYCIDPKLKWIOE 60  
 DB 1 KPVSLSYRCPCRFESHVARANVHKILINPNCALQIVARLKNNNROYCIDPKLKWIOE 60

QY 61 YLEKALN 67  
 DB 61 YLEKALN 67

## RESULT 8

AAV06726  
 ID AAV06726 standard; protein; 67 AA.

XX AAV06726;

DT 18-JUN-1999 (first entry)

XX Amino acid fragment of SDF-1 alpha.

DE Chemokine; cross-over protein; pharmaceutical; inflammatory; AIDS; viral;  
 XX Infectious disease; hematopoiesis; chemoprotection; asthma; RANTES; VMP;  
 KW allergic rhinitis; atopic dermatitis; rheumatoid arthritis; SDF-1; MPAV;  
 KM stromal cell derived factor 1; Macrophage inflammatory protein.

XX Homo sapiens.

OS Synthetic.

XX WO9911655-A1.

XX 11-MAR-1999.

XX 31-AUG-1998; 98WO-US18096.

XX 04-SEP-1997; 97US-0057620.

XX (GRYP-) GRYPHON SCI.

XX Kent SBH, Stanl MA, Simon R, Wilken J;

XX WPI; 1999-205128/17.

PT New cross-over proteins for treatment of inflammation and infections  
 PT e.g. AIDS - prepared by ligation of two functional protein modules  
 PT derived from two different parent molecules

XX Example 4; Page 41; 75pp; English.

CC The invention relates to a cross-over protein produced by chemical  
 CC ligation of at least two functional protein modules derived from at least  
 CC two parent protein molecules. The cross-over proteins can be used in  
 CC pharmaceutical compositions for therapy of inflammatory and infectious  
 CC diseases including AIDS, and for indications of hematopoiesis and  
 CC chemoprotection. They are also useful for treatment of asthma, allergic  
 CC rhinitis, atopic dermatitis and rheumatoid arthritis. A library  
 CC comprising a collection of cross-over proteins is useful for screening  
 CC for cross-over proteins that are receptor ligands. The libraries comprise  
 CC functionally diverse compounds therefore improving the drug discovery  
 CC process. The proteins and libraries are exemplified by the preparation  
 CC of cross-over chemokines comprising various combinations of peptide  
 CC segments derived from RANTES, SDF-1 (stromal cell derived factor 1), VMP  
 CC (Viral Macrophage Inflammatory protein) and other such chemokines. The  
 CC present sequence represents an amino acid fragment of SDF-1 alpha which  
 CC acts as a synthetic base molecule for synthesizing the cross-over  
 CC protein.

SO Sequence 67 AA:

Query Match 97.8%; Score 351; DB 20; Length 67;

Best Local Similarity 98.5%; Pred. No. 1.4e-38;  
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSLSYRCPCRFESHVARANKHLKILTPNCALOIVARLKNNNRQVCIDPKLKWIOE 60  
 DB 1 KVSLSYRCPCRFESHVARANKHLKILTPNCALOIVARLKNNNRQVCIDPKLKWIOE 60  
 QY 61 YLEKALN 67

DB 61 YLEKALN 67

## RESULT 9

AAV67594  
 ID AAV67594 standard; peptide; 67 AA.

XX AAV67594;

DT 13-JUN-2000 (first entry)

XX SDF-1alpha peptide sequence.

DE SDF-1; CXCR4; CXCR4 chemokine receptor 4; gamma-interferon; cancer; gout;  
 KW autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;  
 KW type 1 diabetes; ulcerative colitis; lupus; antagonist; antitumor;  
 KM stromal cell derived factor one; anti-inflammatory; immunomodulatory.

XX Unidentified.

XX WO200009152-A1.

XX 24-FEB-2000.

XX 16-AUG-1999; 99WO-CA00750.

XX 14-AUG-1998; 98CA-2245224.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Clark-Lewis I, Gong J, Duronio V, Salari H;

XX WPI; 2000-224175/19.

PT Therapeutic composition containing CXCR4 antagonist, useful for  
 PT treating autoimmune disease, especially multiple sclerosis and cancer

XX Disclosure: Fig 1; 88pp; English.

CC The invention provides a therapeutic composition containing an antagonist  
 CC of CXCR4 (CXCR4 chemokine receptor 4) and an excipient. The compositions  
 CC are specifically used: to reduce production of gamma-interferon by T  
 CC cells, particularly for treating autoimmune disease, especially multiple  
 CC sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral  
 CC sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative  
 CC colitis, gout, lupus and transplant rejection; to treat cancer by  
 CC inhibiting angiogenesis; inhibition of restenosis; and when labeled, to  
 CC evaluate in vivo pharmacokinetics, or to determine disease progression  
 CC and susceptibility, or as targeting agents for delivery of other  
 CC therapeutic agents. The antagonist is selected from SDF-1 (stromal cell  
 CC derived factor one) peptide fragments, SDF-1 being the only known natural  
 CC ligand for CXCR4. The present sequence represents a SDF-1alpha  
 CC peptide sequence.

SO Sequence 67 AA:

Query Match 97.8%; Score 351; DB 21; Length 67;

Best Local Similarity 98.5%; Pred. No. 1.4e-38;  
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVSLSYRCPCRFESHVARANKHLKILTPNCALOIVARLKNNNRQVCIDPKLKWIOE 60  
 DB 1 KVSLSYRCPCRFESHVARANKHLKILTPNCALOIVARLKNNNRQVCIDPKLKWIOE 60  
 QY 61 YLEKALN 67  
 DB 61 YLEKALN 67  
 RESULT 10  
 AAB47680

ID	AA047680 standard; peptide; 67 AA.
XX	
AC	AA047680:
XX	
DT	30-JAN-2002 (first entry)
XX	
DE	SDF-1-alpha.
XX	
KW	Hematopoietic cell; multiplication; CXCR chemokine receptor 4; CXCR4;
KW	agonist; stromal cell derived factor one; SDF-1; autoimmune disease;
KM	macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;
KW	autologous; allogenic; bone marrow; stem cell; transplantation.
OS	
XX	
PN	Homo sapiens.
XX	
MO	MO200176615-A2.
XX	
PD	18-OCT-2001.
XX	
XX	
PF	12-APR-2001; 2001WO-CO0540.
XX	
PR	12-APR-2000; 2000CA-2305036.
PR	14-SEP-2000; 2000US-232425P.
PR	23-FEB-2001; 2001CA-2335109.
XX	
PA	(UYBR-) UNIV BRITISH COLUMBIA.
PA	(CHEM-) CHEMOKINE THERAPEUTICS CORP.
PI	
PI	Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;
PI	Cashman J, Clark-Lewis I;
DR	WPI; 2002-025882/03.
XX	
CX	CXC receptor 4 agonists that reduces hematopoietic cell multiplication
PT	and susceptibility to cytotoxic agents, are useful for bone marrow or
PT	peripheral blood stem cell transplantation -
PS	Claim 8; Page 57; 74pp; English.
XX	
CC	The sequences given in AA047680-717 represent peptides which may be
CC	used in the method of the invention for reducing the rate of
CC	hematopoietic cell multiplication. These peptides act as CXCR chemokine
CC	receptor 4 (CXCR4) agonists to the cells. These peptides are based on
CC	stromal cell derived factor one (SDF-1) with some also containing
CC	sequences derived from macrophage inflammatory protein 1-alpha
CC	(MIP-1-alpha). They can be used to reduce susceptibility of
CC	hematopoietic cells to a cytotoxic agent, by administering one of the
CC	agonist peptides to the cells prior to or during exposure of the
CC	cells to the cytotoxic agent. The CXCR4 agonist is used to reduce
CC	susceptibility of hematopoietic cells to a cytotoxic agent, particularly
CC	in a patient with cancer requiring autologous or allogeneic bone marrow
CC	or peripheral blood stem cell transplantation, or an autoimmune disease.
XX	
SO	Sequence 67 AA:
XX	
Query Match	97.8%; Score 351; DB 23; Length 67;
Best Local Similarity	98.5%; Pred. No.1,4e-38;
Matches 66; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	1 KGVSLSYRCPCFFESHVARAWKHLKITNPNCALQIIVARLKNRRQVCIPKLKIOWE 60   Db 1 KPVSLSYRCPCRFESHVARAWKHKLKITNPNCALQIIVARLKNRRQVCIDPKLKIOE 60   OY 61 YLEKALN 67   Db 61 YLEKALN 67
RESULT 11	
AAW50761	
ID	AAW50761 standard; peptide; 68 AA.
XX	
CC	AAW50761;

XX	27-JUL-1998	(first entry)
DT		
XX	Peptide which binds to CXCR4 receptor and is useful for treating HIV.	
XX		
XX	Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus;	
KW	HIV, CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.	
XX		
OS	Homo sapiens.	
XX		
PN	FR2751658-A1.	
PD	30-JAN-1998.	
XX		
PF	26-JUL-1996; 96FR-0009477.	
XX		
PR	26-JUL-1996; 96FR-0009477.	
XX		
PA	(INSP ) INST PASTEUR.	
XX		
PI	Arenzana SF, Baggiolini M, Clark LJ, Moser B, Virelizier JL;	
XX		
DR	WPI, 1998-123039/12.	
XX		
PT	Human stromal cell-derived chemokine, SDF-1 - useful for treating	
XX	human immunodeficiency virus infection	
PS		
XX	Claim 5; Page 29; 48pp; French.	
CC		
CC	The invention relates to peptides which bind to a cellular receptor for	
CC	CXC chemokines, namely the CXCR4 receptor (also known as leukocyte-	
CC	expressed transmembrane domain receptor), especially where the	
CC	peptide is human chemokine SDF-1. The peptide can be used to treat or	
CC	prevent HIV infections, optionally together with reverse transcriptase	
CC	inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4	
CC	receptor antagonists, immunotherapy agents, agents for treating HIV-	
CC	associated opportunistic infections and/or other CXC or CC chemokines,	
CC	especially RANTES, MIP1- $\alpha$ , MIP1- $\beta$ or MCP1. The peptide can be	
CC	used to detect anti-SDF-1 antibodies in biological fluids. This	
CC	sequence represents a specifically claimed peptide which binds to the	
CC	CXCR4 receptor.	
XX		
XX	Sequence 68 AA;	
SO		
	Query Match 97.8%; Score 351; DB 19; Length 68;	
	Best Local Similarity 98.5%; Pred. No. 1,4e-38;	
	Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
OY	1 KGVSLSYRCRCFFEEHVARANKHLKILTPNCALQIVARLKNNNOVCIDPKLKWIOE 60	
-db		
	2 KPVSLSRCRCFFEEHVARANKHLKILTPNCALQIVARLKNNNOVCIDPKLKWIOE 61	
OY	61 YLEKALN 67	
Db	62 YLEKALN 68	
XX		
AC	AAV05818;	
XX		
ID	AAV05818 standard; Protein; 69 AA.	
XX		
DT	02-AUG-1999 (first entry)	
XX		
DE	N-terminal modified chemokine met-hSDF-1 alpha.	
XX		
KW	Stromal cell-derived factor 1 alpha; SDF-1 alpha; met-hSDF-1 alpha;	
KW	human; protein engineering; amino-terminal modification; mutant;	
KW	HIV; infection; angiogenesis; autoimmune disease; inflammation;	
KW	antiangiogenic; antiinflammatory; immunosuppressive; therapy;	
KW	vaccine.	
XX		

OS	Homo sapiens.
OS	Synthetic.
PN	MO9920759-AI.
XX	
PD	29-APR-1999.
XX	
PF	21-OCT-1998; 98WO-US22282.
XX	
PR	20-OCT-1998; 98US-0175713.
PR	22-OCT-1997; 97US-0955826.
PR	27-FEB-1998; 98WO-US04002.
XX	
PA	(GEMV ) GENETICS INST INC.
PI	Herrmann SH, Lu Z, McCoy JM, Swanberg SL, Walker B;
PI	Yang O;
XX	
DR	WPI: 1999-288307/24.
DR	N-PSDB; AAX25530.
XX	
PT	Modified chemokines useful for inhibiting or stimulating
PT	angiogenesis
XX	
PS	ClaIm 6c; Page 79; 85pp: English.
XX	
CC	The present sequence represents met-hSDF-1 alpha, i.e. human
CC	stromal cell derived growth factor-1 alpha having an added
CC	N-terminal methionine residue. DNA encoding met-hSDF-1 alpha (see
CC	AAZ5350) was produced by cloning an NdeI/XbaI-restricted hSDF-1
CC	alpha PCR product into the E. coli expression vector pAL781
CC	in-frame with an ATG codon. met-hSDF-1 alpha is an example of
CC	novel N-terminal modified chemokines (see AA05818-21) that have at
CC	least one Met residue, at least one aminoxyphenylamine residue or at
CC	least one GroHEK peptide (see AA05822) covalently attached at the
CC	N-terminus. The N-terminal modified chemokines are useful for
CC	altering receptor function, inhibiting interactions between
CC	chemokine receptors and their ligands. They are used as research
CC	tools for identifying chemokine receptors, as vaccine adjuvants, as
CC	agents for the chemotactic recruitment of migratory cells, as agents
CC	for the stimulation or inhibition of inflammation, as agents against
CC	autoimmune diseases and inflammation, and as agents to inhibit the
CC	binding of HIV to certain receptors and the infection of
CC	susceptible cells by HIV. HIV infection is best treated with
CC	modified SDF-1 alpha and beta or MIP-1 alpha and beta.
XX	
SQ	Sequence 69 AA:
	Query Match 97.8%; Score 351; DB 20; Length 69;
	Best Local Similarity 98.5%; Pred. No. 1,4e-38;
	Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	1 KGVSLSYRCPCRFEESSHARAVNHKLILINPNCALQIVARLKNRRNROYCIDPKLKWIOE 60   Db 2 KPVSLSYRCPCRFEESSHVARANVRKHKLITLPNCALQIVARLKNRRNROYCIDPKLKWIDE 61
OY	61 YLEKALN 67               Db 62 YLEKALN 68
	RESULT 13
ID	AAWS0762
XX	AAWS0762 standard; peptide: 72 AA.
XX	
AC	AAWS0762;
XX	
DT	27-JUL-1998 (first entry)
XX	
DE	Peptide which binds to CXCR4 receptor and is useful for treating HIV.
XX	
KW	Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus;
RN	HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.

XX	Homo sapiens.
OS	FR2751658-A1.
XX	30-JAN-1998.
XX	26-JUL-1996; 96FR-0009477.
XX	26-JUL-1996; 96FR-0009477.
XX	(INSP ) INST PASTEUR.
PI	Arenzana SF, Baggiolini M, Clark LI, Moser B, Virelizier JL;
DR	WPI: 1998-123039/12.
XX	Human stromal cell-derived chemokine, SDF-1 - useful for treating
P7	human immunodeficiency virus infection
PS	Claim 5; Page 29; 48pp; French.
XX	The invention relates to peptides which bind to a cellular receptor for
CC	CXC chemokines, namely the CXCR4 receptor (also known as leukocyte-
CC	expressed transmembrane domain receptor), especially where the
CC	peptide is human chemokine SDF-1. The peptide can be used to treat or
CC	prevent HIV infections, optionally together with reverse transcriptase
CC	inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4
CC	receptor antagonists, immunotherapy agents, agents for treating HIV-
CC	associated opportunistic infections and/or other CXC or CC chemokines,
CC	especially RANTES, MIP1-alpha , MIP1-beta or MCP1. The peptide can be
CC	used to detect anti-SDF-1 antibodies in biological fluids. This
CC	sequence represents a specifically claimed peptide which binds to the
XX	CXCR4 receptor.
SO	Sequence    72 AA:
	Query Match                  97.8%; Score 351; DB 19; Length 72; Best Local Similarity         98.5%; Pred. No. 1.5e-38; Matches    66; Conservative    0; Mismatches    1; Indels      0; Gaps      0;
OY	1 KGVSLSYGCPCEFFESHVAAAVNKKHLKILTPNCALQIVARLKNRRVCIDPKLKWOE 60   Db    1 KPVSLSYRCPCEFESHHVAARVNKKHLKILTPNCALQIVARLNRRVCIDPKLKWOE 60
OY	61 YLEKALN 67           Db    61 YLEKALN 67
RESULT 14	
AAAY34093	
ID AAY34093	standard; protein: 72 AA.
XX	AAAY34093;
XX	Native stromal cell derived factor 1 (SDF-1) beta protein.
D7	29-NOV-1999 (first entry)
DE	CXC chemokine receptor 4; CXCR4; antagonist; medicament; T-cell;
KW	interferon gamma; autoimmune disease; multiple sclerosis; cancer;
KM	angiogenesis; stromal cell derived factor 1; SDF-1.
XX	Mammalia.
OS	MAMMALIA.
XX	MO9947158-A2.
PN	23-SEP-1999.
PD	12-MAR-1999; 99WO-CA00221.
PF	13-MAR-1998; 98CA-2226391.

PR 14-AUG-1998; 98CA-2245224.  
XX  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
XX  
PI Clark-Lewis I, Gong J, Duroonio V;  
XX  
XX WPI: 1999-561857/47.  
DR  
XX  
PT Use of CXCR4 chemokine receptor 4 for treating autoimmune disease and  
XX cancer -  
PS Example 1: Fig 1: 71pp: English.  
XX  
XX The invention relates to the use of a CXCR4 chemokine receptor 4 (CXCR4)  
CC antagonist for the manufacture of a medicament for reducing interferon  
CC gamma production by T-cells in a mammal. The CXCR4 antagonist can be used  
CC to treat or to design a medicament to treat, an autoimmune disease.  
CC multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4  
CC antagonists may be peptide compounds comprising a substantially purified  
CC peptide fragment, analogue or a pharmacologically acceptable salt of  
CC stromal cell derived factor 1 (SDF-1). The present sequence represents  
XX the amino acid sequence of SDF-1 beta protein.  
SQ Sequence 72 AA:  
Query Match 97.8%; Score 351; DB 20; Length 72;  
Best Local Similarity 98.5%; Pred. No. 1.5e-38;  
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KGVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
Db 1 KPVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
QY 61 YLEKALN 67  
Db 61 YLEKALN 67  
RESULT 15  
AAV67595  
ID AAV67595 standard; peptide: 72 AA.  
XX  
AC AAV67595;  
XX  
DT 13-JUN-2000 (first entry)  
XX  
DE SDF-1beta peptide sequence.  
XX  
XX SDF-1; CXCR4; CXCR4 chemokine receptor 4; gamma-interferon; cancer; gout;  
KW autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;  
KW type 1 diabetes; ulcerative colitis; lupus; antagonist; antitumour;  
KW stromal cell derived factor one; anti-inflammatory; immunomodulatory.  
XX  
OS Unidentified.  
XX  
XX WO200009152-A1.  
XX  
XX 24-FEB-2000.  
XX  
XX 16-AUG-1999; 99WO-CA00750.  
XX  
XX 14-AUG-1998; 98CA-2245224.  
XX  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
XX  
XX  
PI Clark-Lewis I, Gong J, Duroonio V, Salari H;  
XX  
XX WPI: 2000-224175/19.  
XX  
XX Therapeutic composition containing CXCR4 antagonist, useful for  
PT treating autoimmune disease, especially multiple sclerosis and cancer  
XX

PS Disclosure; Fig 1; 88pp: English.  
XX  
XX The invention provides a therapeutic composition containing an antagonist  
CC of CXCR4 (CXCR4 chemokine receptor 4) and an excipient. The compositions  
CC are specifically used: to reduce production of gamma-interferon by T  
CC cells, particularly for treating autoimmune disease, especially multiple  
CC sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral  
CC sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative  
CC colitis, gout, lupus and transplant rejection; to treat cancer by  
CC inhibiting angiogenesis; inhibition of restenosis; and when labeled, to  
CC evaluate in vivo pharmacokinetics, or to determine disease progression  
CC and susceptibility, or as targeting agents for delivery of other  
CC therapeutic agents. The antagonist is selected from SDF-1 (stromal cell  
CC derived factor one) peptide fragments, SDF-1 being the only known natural  
CC ligand for CXCR4. The present sequence represents a SDF-1beta  
XX peptide sequence.  
SQ Sequence 72 AA:  
Query Match 97.8%; Score 351; DB 21; Length 72;  
Best Local Similarity 98.5%; Pred. No. 1.5e-38;  
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KGVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
Db 1 KPVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
QY 61 YLEKALN 67  
Db 61 YLEKALN 67  
Search completed: January 23, 2003, 15:33:41  
Job time : 29.2 secs







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: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: JP 280505/1993  
: FILING DATE: 14-OCT-1993  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (202)293-7060  
: TELEFAX: (202)293-7860  
: TELEX: 6491103  
: INFORMATION FOR SEQ ID NO: 5:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 93 amino acids  
: type: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: OS=08-6174-008-5
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Query Match	97.8%	Score 351	DB 1	Length 93
Best Local Similarity	98.5%	Pred. No. 6	4e-39	
Matches 66	Conservative	0	Mismatches 1	Indels 0
				Gaps 0

**Oy** 1 KGVLSIYRCPREFESHVARANKHLKILNTPNCALQIVARKNNROYCIDPKLWIOE 600  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
**Db** 22 KPVSLSYRCPRFESHVARANKHLKILNTPNCALQIVAREKNNRQCIDPKLWIOE 811

OY	61 YLEKALN 67
Db	82 YLEKALN 88

RESULT 5  
US-08-808-720-3  
; Sequence 3, Application US/08808720  
; Patent No. 6100287

Query Match	97.8%	Score 351	DB 3	Length 326
Best Local Similarity	98.5%	Pred. No.	2.9e-38	
Matches	66	Conservative	0	Mismatches 1
				Indels 0
				Gaps 0

[illegible]

RESULT 6  
US-08-808-720-1  
; Sequence 1, Application US/08808720  
; Patent No. 6100387

```

Query Match          97.88; Score 351; DB 3: Length 328;
Best Local Similarity 96.58; Pred. No. 2.9e-38;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY      1 KGVSLSTRCPCRFPEFSHVARANVKKLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIDE 60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       22 KPVSLSYRCPCRFPEFSHVARANVKKLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIDE 81

QY      61 YLEKALN 67
        ||| | | | |
Db       82 YLEKALN 88

RESULT 7
US-08-181-556-2
: Sequence 2, Application US/08181556
: Patent No. 5525486
GENERAL INFORMATION:
: APPLICANT: HONJO, Tasuku
: APPLICANT: TASHIRO, Kei
APPLICANT: TADA, Hideaki
```





ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/244,702  
FILING DATE: 27-SEP-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/CA92/00528  
FILING DATE: 03-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,578  
FILING DATE: 04-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 8080-0004.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-244-702-9

Query Match 26.2%; Score 94; DB 1; Length 68;  
Best Local Similarity 32.3%; Pred. No. 2.6e-05;  
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

QY 8 RCPC-REFESHVAVANKHKLINT-PNCA-LQIVARLKNNNRQVCIDPKLWIOEYLER 64  
DB 2 RCQCICKTYSRPHFKFKELRVIESGPHCANTETIVRL-SDGRRLCIDPKENWVQRYVER 60  
QY 65 AL 66  
DB 61 FL 62

RESULT 13  
US-08-244-702-10  
Sequence 10, Application US/08244702  
Patent No. 5665346  
GENERAL INFORMATION:  
APPLICANT: Clark-Lewis, Ian  
SOFTWARE: Patentin Release #1.0, Version #1.25  
TITLE OF INVENTION: Human Interleukin-8 Analogs  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morlison & Foerster  
STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/244,702  
FILING DATE: 27-SEP-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/CA92/00528  
FILING DATE: 03-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,578

FILING DATE: 04-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 8080-0004.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-244-702-10

Query Match 26.2%; Score 94; DB 1; Length 68;  
Best Local Similarity 32.3%; Pred. No. 2.6e-05;  
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

QY 8 RCPC-REFESHVAVANKHKLINT-PNCA-LQIVARLKNNNRQVCIDPKLWIOEYLER 64  
DB 2 RCQCICKTYSRPHFKFKELRVIESGPHCANTETIVRL-SDGRRLCIDPKENWVQRYVER 60  
QY 65 AL 66  
DB 61 FL 62

RESULT 14  
US-08-244-702-11  
Sequence 11, Application US/08244702  
Patent No. 5665346  
GENERAL INFORMATION:  
APPLICANT: Clark-Lewis, Ian  
SOFTWARE: Patentin Release #1.0, Version #1.25  
TITLE OF INVENTION: Human Interleukin-8 Analogs  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morlison & Foerster  
STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/244,702  
FILING DATE: 27-SEP-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/CA92/00528  
FILING DATE: 03-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,578  
FILING DATE: 04-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 8080-0004.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-244-702-11

Query Match 26.2%; Score 94; DB 1; Length 68;  
Best Local Similarity 32.3%; Pred. No. 2.6e-05;  
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

QY 8 RCPC-REFESHVAVRANKHLKILNT-PNCA-LQIVARLKNNNROVCIDPKLKIQLEYL 64  
DB 2 RCOCIKITYSKPFPKPKIKELRVIESGPHCANTEIIVKL-SDGRELCIDPKENNVQRYVER 60

QY 65 AL 66  
DB 61 FL 62

## RESULT 15

US-08-244-702-2  
Sequence 2, Application US/08244702  
Patent No. 5665346  
GENERAL INFORMATION:  
APPLICANT: Clark-Lewis, Ian  
APPLICANT: Moser, Bernhard  
TITLE OF INVENTION: Human Interleukin-8 Analogs  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/244,702  
FILING DATE: 27-SEP-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/CA92/00528  
FILING DATE: 03-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,578  
FILING DATE: 04-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 8080-0004.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 69 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-244-702-2

Query Match 26.2%; Score 94; DB 1; Length 69;  
Best Local Similarity 32.3%; Pred. No. 2.6e-05;  
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

QY 8 RCPC-REFESHVAVRANKHLKILNT-PNCA-LQIVARLKNNNROVCIDPKLKIQLEYL 64  
DB 3 RCOCIKITYSKPFPKPKIKELRVIESGPHCANTEIIVKL-SDGRELCIDPKENNVQRYVER 61

QY 65 AL 66  
DB 62 FL 63



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 23, 2003, 15:31:18 : Search time 6.2 Seconds  
(without alignments)  
218.059 Million cell updates/sec

Title: US-09-852-424-1  
Perfect score: 359  
Sequence: 1 KGVSLSYRCPCRFESHVAR.....QVCIDPKLKIOWEYLEKALN 67

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	359	100.0	67	9	US-09-852-424-1
2	355	98.9	67	9	US-09-852-424-7
3	354	98.6	67	9	US-09-852-424-3
4	354	98.6	67	9	US-09-852-424-6
5	353	98.3	67	9	US-09-852-424-9
6	352	98.1	67	9	US-09-852-424-2
7	352	98.1	67	9	US-09-852-424-5
8	351	97.8	67	9	US-09-852-424-8
9	351	97.8	67	9	US-09-835-107-1
10	351	97.8	67	10	US-09-144-838-8
11	351	97.8	67	10	US-09-144-838-23
12	351	97.8	89	8	US-08-927-939-22
13	351	97.8	89	9	US-09-792-793A-32
14	351	97.8	89	10	US-09-792-793A-32
15	351	97.8	89	10	US-09-953-692-4
16	351	97.8	89	10	US-09-953-717-4
17	351	97.8	93	8	US-08-927-939-56
18	351	97.8	93	9	US-09-835-107-2
19	351	97.8	93	9	US-09-835-107-3
			93	9	US-09-792-793A-93

20	351	97.8	93	10	US-09-144-838-7	Sequence 7, Appl
21	351	97.8	93	10	US-09-919-497-95	Sequence 95, Appl
22	351	97.8	320	9	US-09-792-793A-77	Sequence 77, Appl
23	351	97.8	322	9	US-09-792-793A-78	Sequence 78, Appl
24	351	97.8	327	9	US-09-792-793A-79	Sequence 79, Appl
25	349	97.2	67	9	US-09-852-424-4	Sequence 4, Appl
26	340.5	94.8	66	9	US-09-852-424-10	Sequence 10, Appl
27	337.5	94.0	66	9	US-09-852-424-11	Sequence 11, Appl
28	335.5	93.5	66	9	US-09-852-424-12	Sequence 12, Appl
29	333.5	92.9	66	10	US-09-144-838-27	Sequence 27, Appl
30	320	89.1	68	10	US-09-144-838-51	Sequence 51, Appl
31	304	84.7	67	10	US-09-144-838-53	Sequence 47, Appl
32	300	83.6	68	10	US-09-144-838-24	Sequence 24, Appl
33	297	82.7	67	10	US-09-144-838-25	Sequence 25, Appl
34	282.5	78.7	67	10	US-09-144-838-28	Sequence 28, Appl
35	269	74.9	69	10	US-09-144-838-52	Sequence 52, Appl
36	266	74.1	68	10	US-09-144-838-53	Sequence 53, Appl
37	259.5	72.3	66	10	US-09-144-838-29	Sequence 29, Appl
38	253	70.5	68	10	US-09-144-838-48	Sequence 48, Appl
39	250	69.6	67	10	US-09-144-838-49	Sequence 49, Appl
40	246	68.5	68	10	US-09-144-838-26	Sequence 26, Appl
41	228.5	63.6	67	10	US-09-144-838-30	Sequence 30, Appl
42	228	63.5	67	10	US-09-144-838-31	Sequence 31, Appl
43	217.5	60.6	66	10	US-09-144-838-35	Sequence 35, Appl
44	215	59.9	69	10	US-09-144-838-54	Sequence 54, Appl
45	199	55.4	68	10	US-09-144-838-50	Sequence 50, Appl

## ALIGNMENTS

RESULT 1  
US-09-852-424-1  
; Sequence 1, Application US/09852424  
; Patent No. US20020156034A1  
; GENERAL INFORMATION:  
; APPLICANT: The University of British Columbia; and  
; APPLICANT: Chemokine Therapeutics Corporation  
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
; FILE REFERENCE: 80021-257  
; CURRENT APPLICATION NUMBER: US/09/852,424  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: CA 2,305,787  
; PRIOR FILING DATE: 2000-05-09  
; PRIOR APPLICATION NUMBER: US 60/205,467  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
; OTHER INFORMATION: Laboratory  
US-09-852-424-1

Query Match 100.0%; Score 359; DB 9; Length 67;  
Best local similarity 100.0%; Pred. No. 6.6e-33;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGVSLSYRCPCRFESHVARANKHLKINTPCALQIVARLKNRRQVCIDPKLKIOWE 60  
DB 1 KGVSLSYRCPCRFESHVARANKHLKINTPCALQIVARLKNRRQVCIDPKLKIOWE 60  
OY 61 YEKALN 67  
DB 61 YEKALN 67

RESULT 2  
US-09-852-424-7  
; Sequence 7, Application US/09852424

Patent No. US20020156034A1  
GENERAL INFORMATION:  
APPLICANT: The University of British Columbia; and  
TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: 80021-257  
CURRENT APPLICATION NUMBER: US/09/852,424  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: CA 2,305,787  
PRIOR FILING DATE: 2000-05-09  
PRIOR APPLICATION NUMBER: US 60/205,467  
PRIOR FILING DATE: 2000-05-19  
NUMBER OF SEQ ID NOS: 135  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MUTAGEN  
LOCATION: (6)  
OTHER INFORMATION: Xaa-P\*-proline-amino acid chimera. See page 17 of  
OTHER INFORMATION: disclosure for possible structures for P\*  
OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
US-09-852-424-7

Query Match 98.9%; Score 355; DB 9; Length 67;  
Best Local Similarity 98.5%; Pred. No. 1,8e-32;

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KGVSLSTRCPREFESHVARANVHKILNTPNCALQIVARLKNNNQVCIIDPKLKWIOE 60  
Db 1 KGVSLXRCPCREFESHVARANVHKILNTPNCALQIVARLKNNNQVCIIDPKLKWIOE 60

Qy 61 YLEKALN 67  
Db 61 YLEKALN 67

RESULT 3  
US-09-852-424-3  
Sequence 3, Application US/09852424  
Patent No. US20020156034A1  
GENERAL INFORMATION:  
APPLICANT: The University of British Columbia; and  
TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: 80021-257  
CURRENT APPLICATION NUMBER: US/09/852,424  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: CA 2,305,787  
PRIOR FILING DATE: 2000-05-09  
PRIOR APPLICATION NUMBER: US 60/205,467  
PRIOR FILING DATE: 2000-05-19  
NUMBER OF SEQ ID NOS: 135  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
OTHER INFORMATION: Laboratory  
US-09-852-424-3

Query Match 98.6%; Score 354; DB 9; Length 67;  
Best Local Similarity 98.5%; Pred. No. 2.3e-32;

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KGVSLSTRCPREFESHVARANVHKILNTPNCALQIVARLKNNNQVCIIDPKLKWIOE 60  
Db 1 KGVSLPYRCPCREFESHVARANVHKILNTPNCALQIVARLKNNNQVCIIDPKLKWIOE 60

Qy 61 YLEKALN 67  
Db 61 YLEKALN 67

RESULT 4  
US-09-852-424-6  
Sequence 6, Application US/09852424  
Patent No. US20020156034A1  
GENERAL INFORMATION:  
APPLICANT: The University of British Columbia; and  
TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: 80021-257  
CURRENT APPLICATION NUMBER: US/09/852,424  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: CA 2,305,787  
PRIOR FILING DATE: 2000-05-09  
PRIOR APPLICATION NUMBER: US 60/205,467  
PRIOR FILING DATE: 2000-05-19  
NUMBER OF SEQ ID NOS: 135  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MUTAGEN  
LOCATION: (5)  
OTHER INFORMATION: Xaa-P\*-proline-amino acid chimera. See page 17 of  
OTHER INFORMATION: disclosure for possible structures for P\*  
OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
US-09-852-424-6

Query Match 98.6%; Score 354; DB 9; Length 67;  
Best Local Similarity 98.5%; Pred. No. 2.3e-32;

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KGVSLSTRCPREFESHVARANVHKILNTPNCALQIVARLKNNNQVCIIDPKLKWIOE 60  
Db 1 KGVSLXRCPCREFESHVARANVHKILNTPNCALQIVARLKNNNQVCIIDPKLKWIOE 60

Qy 61 YLEKALN 67  
Db 61 YLEKALN 67

RESULT 5  
US-09-852-424-9  
Sequence 9, Application US/09852424  
Patent No. US20020156034A1  
GENERAL INFORMATION:  
APPLICANT: The University of British Columbia; and  
TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: 80021-257  
CURRENT APPLICATION NUMBER: US/09/852,424  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: CA 2,305,787  
PRIOR FILING DATE: 2000-05-09  
PRIOR APPLICATION NUMBER: US 60/205,467  
PRIOR FILING DATE: 2000-05-19  
NUMBER OF SEQ ID NOS: 135  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MUTAGEN  
LOCATION: (8)



; OTHER INFORMATION: Xaa-P\*-proline-amino acid chimera. See page 17 of  
; OTHER INFORMATION: disclosure for possible structures for P\*  
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
; OTHER INFORMATION: Laboratory  
US-09-852-424-9

Query Match 98.3%; Score 353; DB 9; Length 67;  
Best Local Similarity 98.5%; Pred. No. 3e-32;  
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KGVSLSTYPCPCRFESHVARANVKHLKILNTPNCALQIVARLKNRRVOCIDPKLKWIOE 60  
DB 1 KGVSLSTYPCPCRFESHVARANVKHLKILNTPNCALQIVARLKNRRVOCIDPKLKWIOE 60

OY 61 YLEKALN 67  
DB 61 YLEKALN 67

RESULT 6

US-09-852-424-2  
; Sequence 2, Application US/09852424  
; Patent No. US20020156034A1

; GENERAL INFORMATION:  
; APPLICANT: The University of British Columbia; and  
; APPLICANT: Chemokine Therapeutics Corporation  
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
; FILE REFERENCE: 80021-257  
; CURRENT APPLICATION NUMBER: US/09/852,424  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: CA 2,305,787  
; PRIOR FILING DATE: 2000-05-09  
; PRIOR APPLICATION NUMBER: US 60/205,467  
; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
; OTHER INFORMATION: Laboratory  
US-09-852-424-2

Query Match 98.1%; Score 352; DB 9; Length 67;  
Best Local Similarity 98.5%; Pred. No. 3.9e-32;  
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KGVSLSTYPCPCRFESHVARANVKHLKILNTPNCALQIVARLKNRRVOCIDPKLKWIOE 60  
DB 1 KGVSLSTYPCPCRFESHVARANVKHLKILNTPNCALQIVARLKNRRVOCIDPKLKWIOE 60

OY 61 YLEKALN 67  
DB 61 YLEKALN 67

RESULT 7

US-09-852-424-5  
; Sequence 5, Application US/09852424  
; Patent No. US20020156034A1

; GENERAL INFORMATION:  
; APPLICANT: The University of British Columbia; and  
; APPLICANT: Chemokine Therapeutics Corporation  
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
; FILE REFERENCE: 80021-257  
; CURRENT APPLICATION NUMBER: US/09/852,424  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: CA 2,305,787  
; PRIOR FILING DATE: 2000-05-09  
; PRIOR APPLICATION NUMBER: US 60/205,467  
; PRIOR FILING DATE: 2000-05-19

; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
; OTHER INFORMATION: Laboratory  
US-09-852-424-5

Query Match 98.1%; Score 352; DB 9; Length 67;  
Best Local Similarity 98.5%; Pred. No. 3.9e-32;  
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KGVSLSTYPCPCRFESHVARANVKHLKILNTPNCALQIVARLKNRRVOCIDPKLKWIOE 60  
DB 1 KGVSLSTYPCPCRFESHVARANVKHLKILNTPNCALQIVARLKNRRVOCIDPKLKWIOE 60

OY 61 YLEKALN 67  
DB 61 YLEKALN 67

RESULT 8

US-09-852-424-8  
; Sequence 8, Application US/09852424  
; Patent No. US20020156034A1

; GENERAL INFORMATION:  
; APPLICANT: The University of British Columbia; and  
; APPLICANT: Chemokine Therapeutics Corporation  
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
; FILE REFERENCE: 80021-257  
; CURRENT APPLICATION NUMBER: US/09/852,424  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: CA 2,305,787  
; PRIOR FILING DATE: 2000-05-09  
; PRIOR APPLICATION NUMBER: US 60/205,467  
; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MUTAGEN  
; LOCATION: (7)  
; OTHER INFORMATION: Xaa-P\*-proline-amino acid chimera. See page 17 of  
; OTHER INFORMATION: disclosure for possible structures for P\*  
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
; OTHER INFORMATION: Laboratory  
US-09-852-424-8

Query Match 97.8%; Score 351; DB 9; Length 67;  
Best Local Similarity 98.5%; Pred. No. 5e-32;  
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KGVSLSTYPCPCRFESHVARANVKHLKILNTPNCALQIVARLKNRRVOCIDPKLKWIOE 60  
DB 1 KGVSLSTYPCPCRFESHVARANVKHLKILNTPNCALQIVARLKNRRVOCIDPKLKWIOE 60

OY 61 YLEKALN 67  
DB 61 YLEKALN 67

RESULT 9

US-09-835-107-1  
; Sequence 1, Application US/09835107  
; Patent No. US20020165123A1  
; GENERAL INFORMATION:  
; APPLICANT: Tudan, Christopher R.

```

: APPLICANT: Merzouk, Ahmed
: APPLICANT: Arab, Lakhdar
: APPLICANT: Saxena, Geeta
: APPLICANT: Eaves, Connie J.
: APPLICANT: Cashman, Johanne
: APPLICANT: Clark-Lewis
: APPLICANT: Salari, Hassan
: TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
: FILE REFERENCE: SMAR012
: CURRENT APPLICATION NUMBER: US/09/835,107
: CURRENT FILING DATE: 2001-08-20
: PRIOR APPLICATION NUMBER: CA 2,305,036
: PRIOR FILING DATE: 2000-04-12
: PRIOR APPLICATION NUMBER: US 60/232,425
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: CA 2,335,109
: PRIOR FILING DATE: 2001-02-23
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 67
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: SDF-1 alpha
: US-09-835-107-1

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Query Match	97.8%	Score 351	DB 9	Length 67	
Best Local Similarity	98.5%	Pred. No. 5e-32			
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				Indels	0
				Gaps	0
QY	1	KCVSLSTYRCPCFEFESHVARAVYKHKLIINTPCALQIYARLKNNNROYCIPDKLWIOE	60		
Db	1	KFVSLSTYRCPCFEFESHVARAVYKHKLIINTPCALQIYARLKNNNROYCIPDKLWIOE	60		
QY	61	YLEKALN	67		
Db	61	YLEKALN	67		

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RESULT 10
US-09-144-838-8
Sequence 8, Application US/09144838A
Patent No. US20020051996A1
GENERAL INFORMATION:
APPLICANT: Siani, Michael A.
APPLICANT: Wilken, Jill
APPLICANT: Simon, Reyna
APPLICANT: Kent, Stephen B.H.
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
FILE REFERENCE: GREN-020/01US
CURRENT APPLICATION NUMBER: US/09/144,838A
CURRENT FILING DATE: 1998-08-31
EARLIER APPLICATION NUMBER: US 60/057,620
EARLIER FILING DATE: 1997-09-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 67
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-144-838-8

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Query Match 97.8% Score 351 DB 10, Length 67;  
 Best Local Similarity 98.5% Pred No 5e-33;  
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1 KGVSLSTYPCPCFFESHHAVARANKHLKLLTNPNCALQIYARLKNNNROYCIDPKLTKIOE 60  
 1 |||||  
 1 KPVSLSTYPCPCFFESHHAVARANKHLKLLTNPNCALQIYARLKNNNROYCIDPKLTKIOE 60

QY	61	YLEKALN	67
Db	61	YLEKALN	67

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RESULT 11
US-09-144-838-23
; Sequence 23, Application US/09144838A
; Patent No. US20020051996A1
; GENERAL INFORMATION:
; APPLICANT: Stani, Michael A.
; APPLICANT: Wilken, Jill
; APPLICANT: Simon, Reyna
; APPLICANT: Kent, Stephen B. H.
; TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
; FILE REFERENCE: GFPN-020/01US
; CURRENT APPLICATION NUMBER: US/09/144,838A
; CURRENT FILING DATE: 1998-08-31
; EARLIER APPLICATION NUMBER: US 60/057,620
; EARLIER FILING DATE: 1997-09-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 67
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-144-838-23

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Query Match	351	97.8%	Score	351	DB 10	Length	67
Best Local Similarity	98.5%		Pred. No.	5e-32			
Matches	66	Conservative	0	Mismatches	1	Indels	0
						Gaps	0
QY	1	KGVSLSYSCPGCEPESHVARANVKKLTIINPNCALQIYARLKNNNROYCDIPKLTWQE	60				
DB	1	KPVSLSYRCPGCEPESHVARANVKKLTIINPNCALQIYARLKNNNROYCDIPKLTWQE	60				
QY	61	YLEKALN	67				
DB	61	YLEKALN	67				

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RESULT 12
US-08-927-939-22
; Sequence 22, Application US/08927939
; Patent No. US2001006640A1
; GENERAL INFORMATION:
; APPLICANT: Granger, David J.
; APPLICANT: Tatalick, Lauren Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; FILE OF INVENTION: augment an inflammatory response.
; FILE REFERENCE: 295.022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-927-939-22

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	Query Match	97.8%	Score 351;	DB 8;	Length 89;	
	Best Local Similarity	98.5%;	Pred. No.6-5e-32;			
	Matches	66;	Conservative	0;	Mismatches	1;
					Indels	0;
					Gaps	0;
Oy	1	KGVSLSTYRCPRFFESHVARANVKHLKLTLPNCALQIVARLKNNNROYCIDPKLKWIOE	60			
Dd	22	KPVSLSTYRCPRFFESHVARANVKHLKLTLPNCALQIVARLKNNNROYCIDPKLKWIOE	81			
Oy	61	YLEKALN	67			

DB 82 YLEKALN 88

RESULT 13

US-09-792-793A-32  
; Sequence 32, Application US/09792793A  
; Patent No. US20020168370A1

; GENERAL INFORMATION:

; APPLICANT: McDonald, John R.

; APPLICANT: Coggin, Philip

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND

; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS

; FILE REFERENCE: 25020-601D

; CURRENT APPLICATION NUMBER: US/09/792,793A

; NUMBER OF SEQ ID NOS: 93

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 32

; LENGTH: 89

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE: OTHER INFORMATION: Human Chemokine Polypeptide: Stromal cell-derived

; OTHER INFORMATION: Factor-1-Alpha (SDF-1-Alpha)

; PUBLICATION INFORMATION:

; JOURNAL: Genomics

; VOLUME: 28

; PAGES: 495-500

; DATE: 1995

US-09-792-793A-32

Query Match

Best Local Similarity 97.8%; Score 351; DB 9; Length 89;

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCVSLSYRCPCRFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

DB 22 KCVSLSYRCPCRFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81

QY 61 YLEKALN 67

DB 82 YLEKALN 88

RESULT 14

US-09-953-692-4

; Sequence 4, Application US/09953692

; Patent No. US20020107195A1

; GENERAL INFORMATION:

; APPLICANT: Shalley, Gupta K.

; TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by

; TITLE OF INVENTION: Administering Stromal Cell Derived Factor-1(

; FILE REFERENCE: P50676C1

; CURRENT APPLICATION NUMBER: US/09/953,692

; CURRENT FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: 09/358,624

; PRIOR FILING DATE: 1999-07-21

; PRIOR APPLICATION NUMBER: 60/093,596

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 4

; LENGTH: 89

; TYPE: PRT

; ORGANISM: Human

US-09-953-692-4

Query Match

Best Local Similarity 97.8%; Score 351; DB 10; Length 89;

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCVSLSYRCPCRFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

DB 22 KCVSLSYRCPCRFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81

QY 61 YLEKALN 67

DB 82 YLEKALN 88

RESULT 15

US-09-953-717-4

; Sequence 4, Application US/09953717

; Patent No. US20020107196A1

; GENERAL INFORMATION:

; APPLICANT: Shalley, Gupta K.

; TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by

; TITLE OF INVENTION: Administering Stromal Cell Derived Factor-1(

; FILE REFERENCE: P50676D1

; CURRENT APPLICATION NUMBER: US/09/953,717

; CURRENT FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: 09/358,624

; PRIOR FILING DATE: 1999-07-21

; PRIOR APPLICATION NUMBER: 60/093,596

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 4

; LENGTH: 89

; TYPE: PRT

; ORGANISM: Human

US-09-953-717-4

Query Match

Best Local Similarity 97.8%; Score 351; DB 10; Length 89;

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCVSLSYRCPCRFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

DB 22 KCVSLSYRCPCRFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81

QY 61 YLEKALN 67

DB 82 YLEKALN 88

Search completed: January 23, 2003, 15:38:00

Job time : 6.2 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:31:02 : Search time 11.6 Seconds  
(without alignments)  
555.259 Million cell updates/sec

Title: US-09-852-424-1

Perfect score: 359

Sequence: 1 KGVSLSYRCPCRFESHVAR.....QVCIDPKLKWIGYLEKALN 67

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	351	97.8	93	2	G01540 cytokine SDF-1-beta
2	350	97.5	89	2	A53497 pre-B-cell growth-
3	350	97.5	89	2	I53416 interleukin-8 homo
4	350	97.5	93	2	I81182 cytokine - mouse
5	101	28.1	101	2	I48148 Neutrophil attract
6	98	27.3	95	2	JN0841 Interleukin-8 - do
7	94	26.2	99	2	A37034 Interleukin-8 prec
8	93	25.9	101	2	S42496 Interleukin-8 prec
9	92	25.6	103	2	A53096 Interleukin-8 prec
10	91.5	25.5	96	2	A32954 gro-alpha precursor
11	90.5	25.2	91	1	A46539 monocyte chemotact
12	88.5	24.7	96	2	JN0572 neutrophil chemo-a
13	88	24.5	101	2	I46871 Interleukin-8 - ra
14	88	24.5	120	2	I48147 monocyte chemotact
15	85.5	23.8	91	1	A28815 monocyte chemotact
16	85.5	23.8	100	2	JH0200 macrophage inflamm
17	85	23.7	109	2	A54678 macrophage inflamm
18	82.5	23.0	75	2	A54188 monocyte chemotact
19	81.5	22.7	75	2	B54188 granulocyte chemot
20	81.5	22.7	92	2	I53322 macrophage inflamm
21	81.5	22.7	119	2	S42881 platelet basic pro
22	81	22.6	120	2	JF0177 lymphocyte and mon
23	81	22.6	148	1	A30209 PDGF-inducible JE
24	81	22.6	148	1	S07723 immediate-early se
25	80.5	22.4	100	2	S21467 macrophage inflamm
26	80.5	22.4	100	2	I55614 GRO-gamma inflamm
27	79.5	22.1	107	2	B38290 GRO-gamma precursor
28	79.5	22.1	107	2	A28414 melanoma growth-st
29	78.5	21.9	101	2	B28414 growth-regulated p

#### ALIGNMENTS

30	78.5	21.9	132	2	A57325 C-X-C chemokine LI
31	77.5	21.6	114	2	A55010 neutrophil-activat
32	77.5	21.6	117	2	B44253 alveolar macrophag
33	76.5	21.3	103	2	A26736 transactivator-ind
34	76.5	21.3	103	2	I50417 RSV-induced protei
35	75.5	21.0	870	2	A41130 dystrophin homolog
36	74.5	20.8	96	2	I48099 eotaxin precursor
37	74	20.6	92	2	A32393 macrophage inflamm
38	73.5	20.5	107	2	JH0281 macrophage inflamm
39	72.5	20.2	126	2	A35766 platelet factor 4,
40	72	20.1	96	2	JC2478 eotaxin precursor
41	71.5	19.9	128	1	TGHU beta-thromboglobul
42	70.5	19.6	53	2	I64831 gene KC protein-1
43	70.5	19.6	90	2	S69133 platelet factor 4
44	69.5	19.4	98	2	I59277 Mob-1 rat
45	69.5	19.4	104	1	PFH04A platelet factor 4

RESULT 1  
G01540  
cytokine SDF-1-beta - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 26-Aug-1999  
C:Accession: G01540  
R:Spottila, L.D.  
submitted to the EMBL Data Library, October 1994  
A:Reference number: G07697  
A:Accession: G01540  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-93 <SPO>  
A:Cross-References: EMBL:U16752; NID:q1272194; PID:g571508  
C:Superfamily: beta-thromboglobulin

Query Match 97.8%; Score 351; DB 2; Length 93;  
Best Local Similarity 98.5%; Pred. No. 5.5e-36;  
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 22 KPVSLSYRCPCRFESHVARANKHLINTPNCALQIYARLKNNNROYCIDPKLWIOE 81  
QY 61 YLEKALN 67  
Db 82 YLEKALN 88

RESULT 2  
A53497  
pre-B-cell growth-stimulating factor precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 20-Jun-2000  
C:Accession: A53497; I59582  
R:Nagasawa, T.; Kikutani, H.; Kishimoto, T.  
Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994  
A:Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.  
A:Reference number: A53497; MUID:94181581; PMID:8134392  
A:Accession: A53497  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-89 <NAG>  
A:Cross-References: GB:ID21072; NID:9413905; PID:BA04648.1; PID:9468457  
R:Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T.  
Science 261, 600-603, 1993  
A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I me  
A:Reference number: I59582; MUID:93342488; PMID:8342023  
A:Accession: I59582  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-89 <RES>



## RESULT 7

Interleukin-8 precursor - human  
 A:Accession: A37034  
 A:Alternate names: beta-thromboglobulin-like protein; fibroblast-derived neutrophil-activating factor; monocyte-derived neutrophil-activating factor  
 C:Species: Homo sapiens (man)  
 C:Date: 08-Dec-1992 #sequence\_revision 08-Dec-1992 #text\_change 20-Aug-1999  
 C:Accession: A37034; J10041; A37791; S37634; P10107; A28598; A27488; A39960; A60401; A60370; M143; 1366-1371, 1989  
 R:Murakami, N.; Shiroo, M.; Matsushima, K.  
 J. Immunol. 143, 1366-1371, 1989  
 A:Title: Genomic structure of the human monocyte-derived neutrophil chemotactic factor I  
 A:Reference number: A37034; MUID:89309826; PMID:2663993  
 A:Accession: A37034  
 A:Molecule type: DNA  
 A:Residues: 1-99 <DNA>  
 A:Cross-references: GB:M28130; NID:g186367; PIDN:AA59158.1; PID:g186368  
 A>Note: the authors failed to translate the last thirty-six nucleotides of the second ex  
 R:Matsushima, K.; Morishita, K.; Yoshimura, T.; Laviu, S.; Kobayashi, Y.; Lew, W.; Appell  
 J. Exp. Med. 167, 1883-1893, 1988  
 A:Title: Molecular cloning of a human monocyte-derived neutrophil chemotactic factor (MD  
 A:Reference number: J10041; MUID:88258376; PMID:3260265  
 A:Accession: J10041  
 A:Molecule type: mRNA  
 A:Residues: 1-99 <MAJ>  
 A:Cross-references: EMBL:Y00787; NID:g34518; PIDN:CA68742.1; PID:g34519  
 A:Title: Regulation of the mRNA for monocyte-derived neutrophil-activating peptide in d  
 A:Reference number: A32791; MUID:89313739; PMID:2664463  
 A:Accession: A32791  
 A:Molecule type: mRNA  
 A:Residues: 1-99 <KOW>  
 A:Cross-references: GB:M26383; NID:g188627; PIDN:AA36323.1; PID:g188628  
 R:King, C.H.; Gordon, G.S.; Konieczkowski, M.; Sedor, J.R.  
 submitted to the EMBL Data Library, February 1992  
 A:Reference number: S37634  
 A:Accession: S37634  
 A:Molecule type: protein  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-97 <KIN>  
 A:Cross-references: EMBL:Z11686; NID:g33958; PIDN:CA77745.1; PID:g33959  
 R:Suzuki, K.; Miyasaka, H.; Ota, H.; Yamakawa, Y.; Tagawa, M.; Kuramoto, A.; Mizuno, S.  
 J. Exp. Med. 169, 1895-1901, 1989  
 A:Title: Purification and partial primary sequence of a chemotactic protein for polymorph  
 A:Reference number: P10107; MUID:85279141; PMID:2659722  
 A:Accession: P10107  
 A:Molecule type: protein  
 A:Residues: 23-32, 'XR', '35', 'X', '37-52', 'L', '54' <SUZ>  
 A:Experimental source: lung giant cell carcinoma Lu65C  
 R:Gregory, H.; Young, J.; Schroeder, J.M.; Mrowietz, U.; Christophers, E.  
 Blochem. Biophys. Res. Commun. 151, 883-890, 1988  
 A:Title: Structure determination of a human lymphocyte derived neutrophil activating pep  
 A:Reference number: A28598; MUID:88162914; PMID:3279957  
 A:Accession: A28598  
 A:Molecule type: protein  
 A:Residues: 28-99 <GRE>  
 R:Walt, A.; Peveril, P.; Aschauer, H.; Baggiolini, M.  
 Blochem. Biophys. Res. Commun. 149, 755-761, 1987  
 A:Title: Purification and amino acid sequencing of NAF, a novel neutrophil-activating fa  
 A:Reference number: A27488; MUID:88106502; PMID:3322281  
 A:Accession: A27488  
 A:Molecule type: protein  
 A:Residues: 28-59 <WAL>  
 R:Yoshimura, T.; Matsushima, K.; Tanaka, S.; Robinson, E.A.; Appella, E.; Oppenheim, J.J  
 Proc. Natl. Acad. Sci. U.S.A. 84, 9233-9237, 1987  
 A:Title: Purification of a human monocyte-derived neutrophil chemotactic factor that has  
 A:Reference number: A39960; MUID:88097462; PMID:3480540  
 A:Accession: A39960  
 A:Molecule type: protein  
 A:Residues: 28-69 <YOS>  
 R:Schröder, J.M.; Sticherling, M.; Henneicke, H.H.; Preissner, W.C.; Christophers, E.  
 J. Immunol. 144, 2223-2232, 1990

A:Title: IL-1alpha or tumor necrosis factor-alpha stimulate release of three NAP-1/IL  
 A:Reference number: A60401; MUID:90187866; PMID:2179408  
 A:Accession: A60401  
 A:Molecule type: protein  
 A:Residues: 23-32 <SCH>  
 A:Experimental source: dermal fibroblasts  
 A>Note: a minor component of this material (15%) includes an additional two amino acid  
 R:Van Damme, J.; Decock, B.; Conings, R.; Lenaerts, J.P.; Opdenacker, G.; Billiau, A.  
 Eur. J. Immunol. 19, 1189-1194, 1989  
 A:Title: The chemotactic activity for granulocytes produced by virally infected fibro  
 A:Reference number: A60591; MUID:89338542; PMID:2668011  
 A:Accession: A60591  
 A:Molecule type: protein  
 A:Residues: 23-33, 'X', '35', 'X', '37-42' <VAN>  
 R:Nakagawa, H.; Hatakeyama, S.; Ikeue, A.; Miyai, H.  
 FEBS Lett. 282, 412-414, 1991  
 A:Title: Generation of Interleukin-8 by plasmin from AVLPR-interleukin-8, the human f  
 A:Reference number: S15827; MUID:91243843; PMID:1828038  
 A:Accession: S15827  
 A:Molecule type: protein  
 A:Residues: 23-33, 'X', '35', 'X', '37-47' <FEB>  
 R:Van Damme, J.; Van Beeumen, J.; Conings, R.; Decock, B.; Billiau, A.  
 Eur. J. Biochem. 181, 337-344, 1989  
 A:Title: Purification of granulocyte chemotactic peptide/interleukin-8 reveals N-term  
 A:Reference number: S04216; MUID:89231715; PMID:2523801  
 A:Accession: S04216  
 A:Molecule type: protein  
 A:Residues: 21-67 <VAA>  
 R:Yoshimura, T.; Robinson, E.A.; Appella, E.; Matsushima, K.; Showalter, S.D.; Skeel,  
 M.O. Immunol. 26, 87-93, 1989  
 A:Title: Three forms of monocyte-derived neutrophil chemotactic factor (MDNCF) distin  
 A:Reference number: A60567; MUID:89181632; PMID:2648135  
 A:Accession: A60567  
 A:Molecule type: protein  
 A:Residues: 21-67 <VAA>  
 R:Yoshimura, T.; Robinson, E.A.; Appella, E.; Matsushima, K.; Showalter, S.D.; Skeel,  
 M.O. Immunol. 26, 87-93, 1989  
 A:Title: The forms starting from positions 21, 23, and 28 represented 8%, 47%, and 45%  
 R:Van Damme, J.; Van Beeumen, J.; Opdenacker, G.; Billiau, A.  
 J. Exp. Med. 167, 1364-1376, 1988  
 A:Title: A novel, NH2-terminal sequence-characterized human monokine possessing neut  
 A:Reference number: A60847; MUID:88187604; PMID:3258625  
 A:Accession: A60847  
 A:Molecule type: protein  
 A:Residues: 28-47 <VAA>  
 R:Car, B.D.; Baggiolini, M.; Walz, A.  
 Biochem. J. 275, 581-584, 1991  
 A:Title: Formation of neutrophil-activating peptide 2 from platelet-derived connectiv  
 A:Reference number: S15417; MUID:91248085; PMID:2039437  
 A:Accession: S15417  
 A:Molecule type: protein  
 A:Status: preliminary  
 A:Residues: 28-99 <CAR>  
 R:Golds, E.E.; Mason, P.; Nyirkos, P.  
 Biochem. J. 259, 585-588, 1989  
 A:Title: Inflammatory cytokines induce synthesis and secretion of gro protein and a n  
 A:Reference number: S03975; MUID:89246368; PMID:2655583  
 A:Accession: S03975  
 A:Molecule type: protein  
 A:Residues: 23-46 <GOL>  
 R:Hotta, K.; Hayashi, K.; Ishikawa, J.; Tagawa, M.; Hashimoto, K.; Mizuno, S.; Suzuki  
 Immunol. Lett. 24, 165-170, 1990  
 A:Title: Coding region structure of interleukin-8 gene of human lung giant cell carci  
 A:Reference number: I54560; MUID:90346419; PMID:2200751  
 A:Accession: I54560  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-99 <RES>  
 A:Cross-references: GB:D14283; NID:g219915; PIDN:BA03245.1; PID:g219916  
 R:Schmid, J.; Weisemann, C.  
 J. Immunol. 139, 250-256, 1987  
 A:Title: Induction of mRNA for a serine protease and a beta-thromboglobulin-like prot  
 A:Reference number: I55992; MUID:87224164; PMID:2953813  
 A:Accession: I55992  
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
A:Residues: 1-99 <RE2>  
A:Cross-references: GB:M17017; NID:g179579; PIDN:AAA35611.1; PID:g179580  
R.Kusner, D.J., Luebberts, E.L.; Nowinski, R.J.; Koneczkowski, M.; King, C.H.; Sedor, J.  
Kidney Int. 39, 1240-1244, 1991  
A>Title: Cytokine- and LPS-induced synthesis of interleukin-8 from human mesangial cells  
A:Reference number: I37902; MUID:91374977; PMID:1895676  
A:Accession: I37902  
A>Status: translated from GR/EMBL/DDBU  
A:Molecule type: mRNA  
A:Residues: 1-97 <RE3>  
A:Cross-references: EMBL:Z11686; NID:g33958; PIDN:CAA77745.1; PID:g33959  
R.Alojuni, S.; Gaetnher, H.F.; Mermod, J.J.; Power, C.A.; Bacon, K.B.; Wells, T.N.C.; PR  
Eur. J. Biochem. 227, 328-334, 1995  
A>Title: A fluorescent interleukin-8 receptor probe produced by targeted labelling at t  
A:Reference number: S67519; MUID:95154308; PMID:7851404  
A:Accession: S67519  
A:Molecule type: mRNA  
A:Residues: 1-99 <ALO>  
C:Comment: This secretory protein is chemotactic for polymorphonuclear leukocytes.  
C:Comment: This protein is variably processed at the amino end. The major form differs i  
C:Genetics:  
A:Gene: GDB:IL8  
A:Cross-references: GDB:I20099; OMIM:146930  
A:Map position: 4q13-4q21  
A:Introns: 22/1; 67/2; 95/2  
C:Superfamily: beta-thromboglobulin  
C:Keywords: chemotaxis; cytokine; inflammation  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-99/Product: interleukin-8, minor form #status experimental <MATA>  
F:23-99/Product: interleukin-8, major fibroblast-derived form #status experimental <MAH  
F:28-99/Product: interleukin-8, major lymphocyte/monocyte-derived form #status experimen

Query Match 26.2%; Score 94; DB 2; Length 99;  
Best Local Similarity 32.3%; Pred. No. 0.00024;  
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

Oy 8 RCPC-RFEESHARANVHLKLTNT-PNCA-LQIYARLKNNROYCIDPKLKWIOEYLEK 64  
|||:::||||:::||||:::||||:::||||:::||||  
Db 33 RCQCIRKITSKPHEPRFIKELRVESGPHCANETIIKL-SDGRELCDPCKENWQVRVEK 91

Oy 65 AL 66  
|  
Db 92 FL 93

RESULT 8  
S42496  
interleukin-8 precursor [similarity] - sheep  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 19-Jan-2001  
C:Accession: S42496; I46997  
R.Iegastelots, I.; Greenlund, T.; Arnaud, P.; Morneux, J.F.; Cordier, G.  
submitted to the EMBL Data Library, March 1994  
A:Description: Nucleotide sequence of ovine interleukin 8 cDNA using polymerase chain re  
A:Reference number: S42496  
A:Accession: S42496  
A:Molecule type: mRNA  
A:Residues: 1-101 <LEGS>  
A:Cross-references: EMBL:X78306; NID:g463253; PIDN:CAA55115.1; PID:g463254  
R.Seow, H.F.; Yoshimura, T.; Wood, P.R.; Colditz, I.G.  
Immunol. Cell Biol. 72, 398-405, 1994  
A>Title: Cloning, sequencing, expression and inflammatory activity in skin of ovine inte  
A:Reference number: I46997; MUID:95137691; PMID:7835984  
A:Accession: I46997  
A>Status: preliminary; translated from GR/EMBL/DDBU  
A:Molecule type: mRNA  
A:Residues: 1-101 <SDO>  
A:Cross-references: GB:S74436; NID:g786590; PIDN:AAB33241.1; PID:g786591  
C:Genetics:  
A:Gene: IL-8  
C:Superfamily: beta-thromboglobulin  
C:Keywords: chemotaxis; cytokine; inflammation

```

F:1-20/Domain signal sequence #status predicted <SIG>
F:21-101/Product: interleukin-8 #status predicted <MAT>

Query Match      25.9%; Score 93; DB 2; Length 101;
Best Local Similarity 30.4%; Pred. No. 0.00032;
Matches 21; Conservative 20; Mismatches 20; Indels 8; Gaps 5;

OY 3 VSLSRRCRCRFESFVAAN---VKHLKIINT-PNCA-LQIVARLKNNRQVCDPKLKW 57
    |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 28 MSTELRCCQ--IKTHSTPFHPKFIKELRVIESGPHCENSEITVLV-NGKEVCIDPKKKW 84
    :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

OY 58 IOEYLEKAL 66
    |:|:|:|
DB 85 VQKVVQAF 93

RESULT 9
A:53096
interleukin-8 precursor - pig
N:Alternate names: alveolar macrophage chemotactic factor-I (AMCF-I)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 02-Jun-1995 #sequence.revision 02-Jun-1995 #text.change 19-Jan-2001
C:Accession: A53096; A44253
R:Lin, G.; Pearson, A.E.; Sammurra, R.W.; Zhou, Y.; Baarsch, M.J.; Weiss, D.J.; Murta
J. Biol. Chem. 269, 77-85, 1994
A:Title: Regulation of interleukin-8 expression in porcine alveolar macrophages by ba
A:Reference number: A53096; MUID:94103507; PMID:8276881
A:Accession: A53096
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-103 <LIN>
A:Cross-references: GB:M86923; NID:g164520; PIDN:AA16616.1; PID:g164521
R:Goodman, R.B.; Foster, D.C.; Mathewes, S.L.; Osborn, S.G.; Kuljper, J.L.; Forstrom,
Biochemistry 31, 10483-10490, 1992
A:Title: Molecular cloning of porcine alveolar macrophage-derived neutrophil chemotac
A:Reference number: A44253; MUID:93041741; PMID:1420165
A:Accession: A44253
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-22, 'D', 24-103 <GOO>
A:Cross-references: GB:M9367; NID:g1235611
A:Experimental source: alveolar macrophage
A:Note: sequence extracted from NCBI backbone (NCBIN:117415, NCBIP:117416)
A:Note: the sequence in Genbank entry P1CAMCF1, release 117.0, has been corrected to
C:Keywords: chemotaxis; cytokine; inflammation
C:Superfamily: beta-chromoglobulin
F:1-22/Domain: signal sequence #status predicted <IG>
F:23-103/Product: interleukin-8 #status predicted <MAT>

Query Match      25.6%; Score 92; DB 2; Length 103;
Best Local Similarity 31.8%; Pred. No. 0.00044;
Matches 21; Conservative 18; Mismatches 19; Indels 8; Gaps 5;

OY 3 VSLSRRCRCRFESFVAAN---VKHLKIINT-PNCA-LQIVARLKNNRQVCDPKLKW 57
    |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 28 VSAELRCCQ--INTHSTPFHPKFIKELRVIESGPHCENSEITVLV-NGKEVCIDPKKKW 84
    :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

OY 58 IOEYLE 63
    |:|:|:|
DB 85 VQKVVQ 90

RESULT 10
A:32954
gro-alpha precursor - mouse
N:Alternate names: gro protein; growth regulated protein; melanoma growth-stimulating
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1989 #sequence.revision 20-Oct-1989 #text.change 20-Aug-1999
C:Accession: A32954; JH0081
R:Quenendo, P.; Alberta, J.; Wen, D.; Graycar, J.L.; Derynck, R.; Stiles, C.D.
J. Biol. Chem. 264, 4133-4137, 1989
A:Title: The platelet-derived growth factor-inducible KC gene encodes a secretory pro
A:Reference number: A32954; MUID:89139485; PMID:2917992

```



A:Accession: A32954  
A:Molecule type: mRNA  
A:Residues: 1-96 <COO>  
A:Cross-references: GB:J04596; NID:g201042; PIDN:AAA40131.1; PID:g201043  
R:Aysec, R.P.; MacDonald-Bravo, H.; Mattei, M.G.; Bravo, R.  
Exp. Cell Res. 180, 267-275, 1989  
A>Title: Cloning and sequence of a secretory protein induced by growth factors in mouse  
A:Reference number: JH0081; MUID:99078502; PMID:2909392  
A:Accession: JH0081  
A:Molecule type: mRNA  
A:Residues: 1-96 <RS>  
C:Comment: This protein is basic and lacks threonine, phenylalanine, and tyrosine.  
C:Genetics:  
A:Map position: 5  
C:Superfamily: beta-thromboglobulin  
C:Keywords: extracellular protein  
F:1-24/Domin: signal sequence #status predicted <Sig>  
F:25-96/Product: gro-alpha #status predicted <Mnt>

Query Match 25.5% Score 91.5; DB 2; Length 96;  
Best Local Similarity 32.8%; Pred. No. 0.00047;  
Matches 20; Conservative 17; Mismatches 21; Indels 3; Gaps 3;

Dy 66 L 66  
+  
Dy 91 L 91

RESULT 11  
A46539  
monocyte chemoattractant cytokine RANTES precursor - mouse  
N:Alternate names: MRantes  
C:Species: Mus musculus (house mouse)  
C>Date: 18-Jun-1993 #sequence\_revision 16-Aug-1996 #text\_change 22-Jun-1999  
C:Accession: I48875; A46539; I48654; I56970  
R:Dnoff, T.M.; Falley, P.A.; Cheng, Y.S.; Heeger, P.S.; Neilson, E.G.  
J. Immunol. 152, 1182-1189, 1994  
A>Title: Cloning, genomic organization, and chromosomal localization of the Sca5 gene  
A:Reference number: I48875; MUID:94132613; PMID:7507961  
A:Accession: I48875  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-91 <DNA>  
A:Cross-references: EMBL:U02298; NID:g460090; PIDN:AAI18302.1; PID:g460091  
R:Schall, T.J.; Simpson, N.J.; Mak, J.Y.  
Eur. J. Immunol. 22, 1477-1481, 1992  
A>Title: Molecular cloning and expression of the murine RANTES cytokine: structural and  
A:Reference number: A46539; MUID:92289805; PMID:1376260  
A:Accession: A46539  
A:Molecule type: mRNA  
A:Residues: 1-18, 'A', 20-91 <SCH>  
A:Cross-references: GB:S37648; NID:g250207; PIDN:AAE2330.1; PID:g250208  
A:Experimental source: macrophage cell line PU5-1.8  
A>Note: sequence extracted from NCBI backbone (NCBIR:106768, NCBIP:106770)  
R:Shin, H.S.; Drysdale, B.E.; Shin, M.L.; Noble, P.W.; Fisher, S.N.; Paznekas, W.A.  
Mol. Cell. Biol. 14, 2914-2925, 1994  
A>Title: Definition of a lipopolysaccharide-responsive element in the 5'-flanking region  
A:Reference number: I48654; MUID:94217689; PMID:7513046  
A:Accession: I48654  
A>Status: translation not shown; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-91 <SH>  
A:Cross-references: EMBL:X70675; NID:g475205; PIDN:CAA50011.1; PID:g475206  
R:Nelson, E.G.; Krensky, A.  
Kidney Int. 41, 220-225, 1992  
A>Title: Isolation and characterization of cDNA from renal tubular epithelium encoding p  
A:Reference number: I56970; MUID:92277990; PMID:1375672  
A:Accession: I56970  
A>Status: translated from GB/EMBL/DDBJ

A:Molecule type: mRNA  
A:Residues: 1-40, 'E', 'A2'-91 <NET>  
A:Cross-references: GB:M77747; NID:g200649; PIDN:AAA0029.1; PID:g200650  
C:Comment: This chemoattractant for monocytes but not neutrophils is an immediate-ear  
C:Genetics:  
A:Introns: 26/1; 63/2  
C:Superfamily: macrophage inflammatory protein  
C:Keywords: chemotaxis; cytokine; immediate-early protein; inflammation  
F:1.23/Domain: signal sequence #status predicted <SIG>  
F:24-91/Product: monocytic chemoattractant cytokine RANTES #status predicted <MAT>

Query Match 25.2%; Score 90.5; DB 1: Length 91;  
Best Local Similarity 38.2%; Pred. No. 0.00059;  
Matches 21: Conservative 9; Mismatches 22; Indels 3; Gaps 2;

OY 10 PCRFESHVA--RANVKHLKILNPNCALQIVARIKKNNRVGCIIDPKLKIOWYL 62  
||| : ||| : | : | : ||| : ||| :  
Db 32 PCRPAVLSIALPRAHVKEY-FYTSSCKSNLAIVVEPTRNRNQVCANPEKKWQVEYI 85

RESULT 12  
JN0572  
neutrophil chemo-attractant Gro protein precursor - rat  
N:Alternate names: CINC, cytokine-induced neutrophil chemoattractant; Interleukin-8-1  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Sep-1993 #sequence, revision 30-Sep-1993 #text, change 20-Jun-2000  
C:Accession: JN0572; JQ1519; A34481; A48988; B48988; S51214  
R:Konishi, K.; Takata, Y.; Yamamoto, M.; Yomogida, K.; Tsurufuji, S.; F  
Gene 126, 285-286, 1993  
A>Title: Structure of the gene encoding rat neutrophil chemo-attractant Gro.  
A:Reference number: JN0572; MUID:93246259; PMID:8482545  
A:Accession: JN0572  
A:Molecule type: DNA  
A:Residues: 1-96 <KON>  
A:Cross-references: DDBJ:D11445; NID:g391854; PIDN:BAA02009.1; PID:g220755  
R:Huang, S.; Paulauskis, J.D.; Kobzik, L.  
Biochem. Biophys. Res. Commun. 184, 922-929, 1992  
A>Title: Rat KC cDNA cloning and mRNA expression in lung macrophages and fibroblasts.  
A:Reference number: JQ1519; MUID:92246987; PMID:1374243  
A:Accession: JQ1519  
A:Molecule type: mRNA  
A:Residues: 1-32, 'S', '34'-96 <HUA>  
A:Cross-references: GB:M86536  
A:Experimental source: alveolar macrophage  
A>Note: The authors translated the codon AGT for residue 33 as Cys, AAC for residue 4  
R:Matanabe, K.; Konishi, K.; Fujioaka, M.; Kinoshita, S.; Nakagawa, H.  
J. Biol. Chem. 264, 19559-19563, 1989  
A>Title: The neutrophil chemoattractant produced by the rat kidney epitheloid cell 1  
A:Reference number: A34481; MUID:90062049; PMID:2684956  
A:Accession: A34481  
A:Molecule type: protein  
A:Residues: 25-96 <MAT>  
R:Nakagawa, H.; Ikeue, A.; Hatakeyama, S.; Kato, H.; Gotoda, T.; Komorita, N.; Watan  
Biochem. Pharmacol. 45, 1425-1430, 1993  
A>Title: Production of an interleukin-8-like chemokine by cytokine-stimulated rat NRK  
A:Reference number: A48988; MUID:93228656; PMID:8471066  
A:Accession: A48988  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 25-57 <NAK>  
A:Experimental source: kidney, NRK-49F fibroblasts  
A>Note: sequence extracted from NCBI backbone (NCBIP:129132)  
A:Accession: B48988  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 25-57 <NA2>  
A:Experimental source: kidney, NRK-49F fibroblasts  
A>Note: sequence extracted from NCBI backbone (NCBIP:129131)  
R:Hanzawa, H.; Haruyama, H.; Watanabe, K.; Tsurufuji, S.  
FEBS Lett. 354, 207-212, 1994  
A>Title: The three dimensional structure of rat cyclokin CINC/Gro in solution by homo  
A:Reference number: S51214; MUID:95046335; PMID:7957925  
A:Contents: annotation; conformation by (1)H-NMR, residues 25-96

A:Accession: S51214  
 A:Molecule type: protein  
 A:Residues: 25-96 <HAN>  
 C:Comment: This protein has chemotactic activity for neutrophils and has melanoma growth  
 C:Genetics:  
 A:Gene: gro; KC  
 A:introns: 24/1; 65/2; 92/2  
 C:Superfamily: beta-thromboglobulin  
 C:Keywords: cytokine; disulfide bond  
 F:1-24/Domain: signal sequence #status predicted <Sig>  
 F:25-96/Product: neutrophil chemo-attractant Gro protein #status experimental <Cyt>

Query Match 24.7%; Score 88.5; DB 2; Length 96;  
 Best Local Similarity 30.3%; Pred. No. 0.0011;  
 Matches 20; Conservative 18; Mismatches 25; Indels 3; Gaps 3;

OY 3 VSLSYRCPCEFFESHVARANKHLKIINT-PNCA-LOIVARLKNNNQVCIDPKLKIOE 60  
 DB 27 VANELRCQCLQTVAGLHFNKNIQSLKMPGPHCTQTEVIATLK-NGREACLDPEAPVYOK 85

OY 61 YLEKAL 66  
 DB 86 IVOKML 91

#### RESULT 13

interleukin-8 - rabbit  
 N:Alternate names: neutrophil attractant/activation protein-1  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 20-Aug-1999  
 C:Accession: I46871; S13052  
 R:Yoshimura, T.; Yuhki, N.  
 J:Immunol. 146, 3483-3488, 1991  
 A:Title: Neutrophil attractant/activation protein-1 and monocyte chemoattractant protein  
 A:Reference number: I46871; M0ID:91225489; PMID:2026877  
 A:Accession: I46871  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-101 <ROS>  
 A:Cross-references: GB:M57439; NID:q165552; PIDN:AAA31422.1; PID:q165553  
 R:Beaublein, B.C.; Collins, P.D.; Jose, P.J.; Totly, N.F.; Hsuan, J.; Waterfield, M.D.; W  
 Blochem. J. 271, 797-801, 1990  
 A:Title: A novel neutrophil chemoattractant generated during an inflammatory reaction in  
 Interleukin 8.  
 A:Reference number: S13052; M0ID:91058518; PMID:2244680  
 A:Accession: S13052  
 A:Molecule type: protein  
 A:Residues: 23-33, 'X', '35', 'X', '37-46', 'X', '48-49', 'I', '51-53 <BEA>  
 C:Superfamily: beta-thromboglobulin  
 C:Keywords: cytokine

Query Match 24.5%; Score 88; DB 2; Length 101;  
 Best Local Similarity 28.8%; Pred. No. 0.0013;  
 Matches 19; Conservative 21; Mismatches 18; Indels 8; Gaps 5;

OY 3 VSLSYRCPCEFFESHVARAN---VKHLKIINT-PNCA-LOIVARLKNNNQVCIDPKLKX 57  
 DB 28 IGTLEKQC--IKTHSPFPKRIKELRVIESGPHCANSEIYKLV-DGRELCIDPEKX 84

OY 58 IOEYLE 63  
 DB 85 VOKVQ 90

#### RESULT 14

monocyte chemoattractant protein-1 - guinea pig  
 C:Species: Cavia porcellus (guinea pig)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
 C:Accession: I48147  
 R:Yoshimura, T.  
 J:Immunol. 150, 5025-5032, 1993

A:Title: cDNA cloning of guinea pig monocyte chemoattractant protein-1 and expression  
 A:Reference number: I48147; M0ID:93267104; PMID:8496603  
 A:Accession: I48147  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-120 <RES>  
 A:Cross-references: GB:I04985; NID:q349820; PIDN:AAA37047.1; PID:q349821  
 C:Genetics:  
 A:Gene: MCP-1  
 C:Superfamily: macrophage inflammatory protein

Query Match 24.5%; Score 88; DB 2; Length 120;  
 Best Local Similarity 29.6%; Pred. No. 0.0016;  
 Matches 16; Conservative 10; Mismatches 28; Indels 0; Gaps 0;

OY 11 CRFFESHVARANKHLKIINTPCALQIVARLKNNNQVCIDPKLKIOEYLEK 64  
 DB 34 CYTFNKQIPLRKVGKRYRTSSRCPOEAVIFRLKNEVCADPTQKWVODYIAK 87

#### RESULT 15

monocyte chemoattractant cytokine RANTES precursor - human  
 N:Alternate names: small inducible cytokine A5; T-cell specific cytokine RANTES  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Jun-1989 #sequence\_revision 16-Aug-1996 #text\_change 29-May-1998  
 C:Accession: A28815  
 R:Schall, T.J.; Jonstra, J.; Dyer, B.J.; Jorgensen, J.; Clayberger, C.; Davis, M.M.;  
 J:Immunol. 141, 1018-1025, 1988  
 A:Title: A human T cell-specific molecule is a member of a new gene family.  
 A:Reference number: A28815; M0ID:88285659; PMID:2456327  
 A:Accession: A28815  
 A:Molecule type: mRNA  
 A:Residues: 1-91 <SCH>  
 A:Cross-references: GB:M21121  
 C:Comment: The acronym RANTES reflects the description "Regulated upon Activation, No  
 C:Genetics:  
 A:Gene: GDB:SCYA5; D17S136E  
 A:Cross-references: GDB:120749; OMIM:187011  
 A:Map position: 17q11.2-17q12  
 C:Superfamily: macrophage inflammatory protein  
 C:Keywords: chemotaxis; cytokine; immediate-early protein; inflammation; T-cell  
 F:1-23/Domain: signal sequence #status predicted <Sig>  
 F:24-91/Product: T-cell protein RANTES #status predicted <MAT>

Query Match 23.8%; Score 85.5; DB 1; Length 91;  
 Best Local Similarity 33.9%; Pred. No. 0.0024;  
 Matches 19; Conservative 13; Mismatches 19; Indels 5; Gaps 3;

OY 10 PCRFESHVARANK-HLK--INTPCALQIVARLKNNNQVCIDPKLKIOEYL 62  
 DB 32 PCCF--AVIARPLRAHRIKEYFTSGCKSNPAVVFYRKRRQVCANERKKVAREYI 85

Search completed: January 23, 2003, 15:37:23  
 Job time: 12.6 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 23, 2003, 15:28:07 ; Search time 6 Seconds  
(without alignments)  
463.152 Million cell updates/sec

Title: US-09-852-424-1  
Perfect score: 359  
Sequence: 1 KGVSLSYRCPGCRFFESHVAR.....QVCIDPKLKNIQEYLEKALN 67

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SWISSPROT\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	351	97.8	93	SDFL_FELCA	O62657 felis saplen
2	351	97.8	93	SDFL_HUMAN	P48061 homo sapien
3	350	97.5	89	SDFL_MOUSE	P40224 mus musculu
4	101	28.1	101	IL8_CANFA	P41324 canis famli
5	101	28.1	101	IL8_CANPO	P48113 cavia porce
6	98	27.3	101	IL8_FELCA	O9X5X5 felis silve
7	94	26.2	99	IL8_HUMAN	P10145 h interleuk
8	93	25.9	101	IL8_SHEEP	P36925 ovis aries
9	92	25.6	103	IL8_PIG	P26894 sus scrofa
10	91.5	25.5	96	GRO_MOUSE	P12850 mus musculu
11	91	25.3	101	IL8_MACMO	P31495 macaca mula
12	90.5	25.2	91	SY05_MOUSE	P30882 mus musculu
13	90.5	25.2	92	SY05_RAT	P50231 rattus norv
14	90	25.1	101	IL8_BOVIN	P79255 bos taurus
15	90	25.1	130	SY05_RAT	P97885 rattus norv
16	88.5	24.7	96	GRO_RAT	P14095 rattus norv
17	88	24.5	101	IL8_RABIT	P18874 oryctolagus
18	88	24.5	120	SY02_CANPO	O08782 cavia porce
19	87.5	24.4	91	SY05_CANPO	P97272 cavia porce
20	87	24.2	101	IL8_CERTO	P46653 cercopithec
21	85.5	23.8	50	SY05_PIG	O28288 sus scrofa
22	85.5	23.8	91	SY05_HUMAN	P13501 homo sapien
23	85.5	23.8	100	MIP2_MOUSE	P10889 mus musculu
24	85	23.7	99	SY07_HUMAN	P80098 homo sapien
25	82.5	23.0	114	SZ06_HUMAN	P80162 homo sapien
26	81.5	22.7	71	GRO1_RABIT	P30782 oryctolagus
27	81.5	22.7	92	SY03_RAT	P50229 rattus norv
28	81.5	22.7	112	SY06_BOVIN	P80221 bos taurus
29	81.5	22.7	119	SZ07_PIG	P43030 sus scrofa
30	81	22.6	148	SY02_MOUSE	P10148 mus musculu
31	81	22.6	148	SY02_RAT	P14844 rattus norv
32	80.5	22.4	100	MIP2_RAT	P30348 rattus norv
33	80	22.3	89	SY18_HUMAN	P55774 h small ind

34	80	22.3	120	1	SY16_HUMAN	O15467 h small ind
35	79.5	22.1	107	1	GRO_HUMAN	P09341 homo sapien
36	79.5	22.1	107	1	M12B_HUMAN	P19876 homo sapien
37	78.5	21.9	91	1	SY05_BOVIN	O97919 bos taurus
38	78.5	21.9	97	1	SY08_MOUSE	O92121 mus musculu
39	78.5	21.9	101	1	GRO_CRIGR	P09340 cricetus
40	78.5	21.9	132	1	SZ05_MOUSE	P50328 mus musculu
41	78	21.7	109	1	SZ13_HUMAN	O43927 homo sapien
42	78	21.7	119	1	SY24_MOUSE	O91K00 mus musculu
43	77.5	21.6	114	1	SZ05_HUMAN	P42830 homo sapien
44	77.5	21.6	117	1	AMC2_PIG	P22952 sus scrofa
45	77	21.4	98	1	SY13_HUMAN	O99616 homo sapien

## ALIGNMENTS

```

RESULT 1
SDFL_FELCA
ID SDFL_FELCA STANDARD: PRT: 93 AA.
AC O62657:
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12).
GN SDF1.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RX MEDLINE=96450506; PubMed=9777331;
RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K.,
RA Cai J.S., Sato E., Kohmoto M., Mikami T.;
RT "Molecular cloning and sequencing of feline stromal cell-derived
factor-1 alpha and beta."
RL Eur. J. Immunogenet. 23:303-305(1998).
CC -!- FUNCTION: CHEMOKINE-INDUCED T-LYMPHOCYTES, MONOCYTES, BUT
CC NOT NEUTROPHILS.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE);
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO THE INTERFERIN ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: AB011966; BAA28602.1; -
DR HSSP: P48061; 1SDP.
DR InterPro: IPR001089; CXC_chemkine-smll.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
KW Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 93
FT DISULFID 30 55
FT DISULFID 32 71
FT VARSPPLIC 90 93
FT SEQUENCE 93 AA: 10581 MW: 44RC763711E9B37 CRC64;
Query Match 97.8%; Score 351; DB 1; Length 93;
Best Local Similarity 98.5%; Pred. No. 3.2e-36;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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OY 1 KGVSLSYRCPREFESHVARANVNHKLINTPNCALQIVARLNNNOVCIDPKLKWIOE 60
DB 22 KPVSLSYRCPREFESHVARANVNHKLINTPNCALQIVARLNNNOVCIDPKLKWIOE 81
OY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 2
SDFL_HUMAN
ID SDFL_HUMAN STANDARD: PRT: 93 AA.
AC P48061;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell
DE growth stimulating factor) (PBSF) (hIRH).
GN SDF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Spolia L.D.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96039262; PubMed=7490086;
RA Shirozu M., Nakano T., Inazawa J., Tashiro K., Tada H.,
RA Shinohara T., Honjo T.;
RT "Structure and chromosomal localization of the human stromal cell-
RT derived factor 1 (SDF1) gene."
RL Genomics 28:495-500(1995).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Liver;
RA Begun N.A., Barnard G.F.;
RT "Nucleotide sequence of hIRH, human Interleukin reduced in
RT hepatomas."
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP STRUCTURE BY NMR OF 22-88.
RX MEDLINE=98046030; PubMed=9384579;
RA Crump M.P., Gong J.H., Loetscher P., Rajaratnam K., Amara A.,
RA Arezuma-Seisdedos F., Vitellizier J.L., Baggiolini M., Sykes B.D.,
RA Clark-Lewis I.;
RT "Solution structure and basis for functional activity of stromal
RT cell-derived factor-1; dissociation of CXCR4 activation from binding
RT and inhibition of HIV-1."
RL EMBO J. 16:6996-7007(1997).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-88.
RX MEDLINE=98284037; PubMed=9618518;
RA Dealwis C., Fernandez E.J., Thompson D.A., Simon R.J., Siani M.A.,
RA Lolis E.;
RT "Crystal structure of chemically synthesized [N33A] stromal
RT cell-derived factor 1alpha, a potent ligand for the HIV-1 'fusin'
RT coreceptor."
RL Proc. Natl. Acad. Sci. U.S.A. 95:6941-6946(1998).
RN [6]
RP FUNCTION: CHEMOKINE RECEPTOR ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT
RN NOT NEUTROPHILS.
RN [7]
RP ALTERNATIVE PRODUCTS: 2 ISOFORMS, ALPHA AND BETA (SHOWN HERE);
RN ARE PRODUCED BY ALTERNATIVE SPLICING.
RN [8]
RP SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
RN C-X-C) (CHEMOKINE CXK).
RN [9]
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CC or send an email to license@isb-sib.ch).
DB 22 KPVSLSYRCPREFESHVARANVNHKLINTPNCALQIVARLNNNOVCIDPKLKWIOE 81
OY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 3
SDFL_MOUSE
ID SDFL_MOUSE STANDARD: PRT: 89 AA.
AC P40224;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell
DE growth stimulating factor) (PBSF) (12-O-tetradecanoylphorbol 13-
DE acetate repressed protein 1) (TPAR1) (Thymic lymphoma cell stimulating
DE factor) (TISF).
GN SDF1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94181581; PubMed=8134392;
RA Nagasawa T., Kikutani H., Kishimoto T.;
RT "Molecular cloning and structure of a pre-B-cell growth-stimulating
RT factor."
RL Proc. Natl. Acad. Sci. U.S.A. 91:2305-2309(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93342488; PubMed=8342023;
RA Tashiro K., Tada H., Heilker R., Shirozu M., Nakano T., Honjo T.;
RT "Signal sequence trap: a cloning strategy for secreted proteins and
RT type I membrane proteins."
RL Science 261:600-603(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95073497; PubMed=7982471;
RA Jiang W., Zhou P., Kahn S.M., Tomita N., Johnson M.D.,

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RA  *neurexin 1.B.;
RT  "Molecular cloning of TPRL, a gene whose expression is repressed by
RL  the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA).";
RL  Exp. Cell Res. 215:284-293(1994).
RN  [4]
RP  SEQUENCE FROM N.A.
RC  STRAIN=AKR/J;
RL  Nomura M., Nakata Y., Uezawa A., Nose M., Akashi M., Suzuki G.;
CC  Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC  -1- FUNCTION: CHEMOTACTRACTANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT
CC  NOT NEUTROPHILS.
CC  -1- FUNCTION: STIMULATES THE PROLIFERATION OF BONE MARROW-DERIVED B
CC  PROGENITOR CELLS IN THE PRESENCE OF IL-7 AS WELL AS GROWTH OF THE
CC  STROMAL CELL-DEPENDENT B-CELL CLONE DW4 CELLS.
CC  -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE);
CC  ARE PRODUCED BY ALTERNATIVE SPLICING.
CC  -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC  C-X-C) (CHEMOKINE CXCL).
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; D21072; BAA04648.1; -
DR  EMBL; L12029; AAA40100.1; -
DR  EMBL; L12030; AAA40101.1; -
DR  EMBL; S74318; AAB33650.1; -
DR  EMBL; D43804; BAB07862.1; -
DR  EMBL; D43805; BAA07863.1; -
DR  PIR; A53497; A53497.
DR  HSSP; P48061; 1SDF.
DR  MGD; MGI:103556; Sgfl.
DR  InterPro; IPR001089; CXC-ChmKline_small.
DR  InterPro; IPR001811; Chemokine_IL8.
DR  Pfam; PF00048; IL8; 1.
DR  SMART; SM00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
DR  PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
KW  Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing.
FT  SIGNAL 1 19
FT  CHAIN 1 89
FT  DISULFID 30 55
FT  DISULFID 32 71
FT  VARSPIC 89 89
SQ  SEQUENCE 89 AA: 10032 MW: 10032 MW: CAB8AD69078E55FA CRC64;

Query Match 97.5%; Score 350; DB 1; Length 89;
Best Local Similarity 97.0%; Pred. No. 4e-36;
Matches 65; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KGVSLSTVRCPRPFRESHVAAANVKKLTLNPNKALQIVARLKNNNNROYCDIPKIKWIOE 60
DB 22 KPVSLSTVRCPRPFRESHVAAANVKKLTLNPNKALQIVARLKNNNNROYCDIPKIKWIOE 81
OY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 4
IL8_CANFA
AC PA1324; STANDARD; PRT; 101 AA.
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN IL8.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

CC Mammalia:Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX EMBL\_TextID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94010328; PubMed=7916715;  
RA Ishikawa J., Suzuki S., Hotta K., Hirota Y., Mizuno S., Suzuki K.;  
RT "Cloning of a canine gene homologous to the human  
interleukin-8-encoding gene.";  
RL Gene 131:305-306(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph node;  
RX MEDLINE=95127913; PubMed=7827282;  
RA Matsuno Y., Mohamed A., Onodera T., Kato H., Ohashi T.,  
RA Gotsuno T., Tsujimoto H., Hasegawa A., Furusawa S., Yoshihara K.,  
RA Ishikawa J., Hotta K., Suzuki K., Hirota Y.;  
RT "Molecular cloning and expression of canine Interleukin 8 cDNA.";  
RL Cytokine 6:455-461(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Mongrel; TISSUE=Jugular vein;  
RX MEDLINE=95114148; PubMed=7814650;  
RA Kunkielka G.L., Smith W.C., Larosa G.J., Manning A.M.,  
RA Mendoza L.H., Dally T.J., Hughes B.J., Youker K.A., Hawkins H.K.,  
RA Michael L.H., Rot A., Entman M.L.;  
RT "Interleukin-8 gene induction in the myocardium after ischemia and  
reperfusion in vivo.";  
RL J. Clin. Invest. 95:89-103(1995).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Beagle;  
RX MEDLINE=97230298; PubMed=9119462;  
RA Straubinger R.K., Straubinger A.F., Harter L., Jacobson R.H.,  
RA Chang Y.-F., Summers B.A., Epf H.N., Appel M.J.;  
RT "Borrelia burgdorferi migrates into joint capsules and causes an up-  
regulation of interleukin-8 in synovial membranes of dogs  
experimentally infected with ticks.";  
RL Infect. Immun. 65:1273-1285(1997).  
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,  
BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN  
NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN  
RESPONSE TO AN INFLAMMATORY STIMULUS.  
CC -1- SUBUNIT: HOMODIMER.  
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE  
C-X-C) (CHEMOKINE CX-C).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib.ch](mailto:license@sib.ch)).  
CC -----  
CC EMBL; D28772; BAA05961.1; -;  
DR EMBL; D14285; BAA03246.1; -;  
DR EMBL; U10308; AAC4834.1; -;  
DR EMBL; AF048717; AAC05134.1; -;  
DR HSSP; P10145; 1IKM.  
DR InterPro; IPR001089; CX-C\_chim\_kine\_smll.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR PRINTS; PRO0437; SMALLCYTCXC.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00471; SMALL\_CYTOKINES\_CXC; 1.  
KW Cytokine; Chemotaxis; Inflammatory response; Signal.  
FT SIGNAL 1 22 BY SIMILARITY.  
FT CHAIN 23 101 INTERLEUKIN-8.  
FT DISULFID 34 61 BY SIMILARITY.  
FT DISULFID 36 77 BY SIMILARITY.  
SQ SEQUENCE 101 AA; 11280 MW; 3A3A4676DA968376 CMC64;  
Query Match 28.1%; Score:101; DB 1; Length 101;

Best Local Similarity 36.1%; Pred. No. 1.4e-05;  
Matches 26; Conservative 15; Mismatches 19; Indels 12; Gaps 5;

OY 3 VSLSYRCPREFESHVARAN---VKHLKILNT--PNCA-LOIVARLKNNNROVCIDPKLKW 57  
DB 28 VSSLRQC--IKHTSPFPFKIKELRLVIDSGPHCENSEITIVKL--EVCIDPKRKM 84

OY 58 IOE---YLEKA 65  
DB 85 VQKVEJFLKKA 96

RESULT 5  
IL8\_CAVPO ID IL8\_CAVPO STANDARD; PRT; 101 AA.

AC P49113;  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Interleukin-8 precursor (IL-8) (CXCL8) (Neutrophil attractant protein 1) (NAP-1).  
GN IL8.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
ON NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=94065176; PubMed=7504015;

RA Yoshimura T., Johnson D.G.;  
RT "CDNA cloning and expression of guinea pig neutrophil attractant protein-1 (NAP-1). NAP-1 is highly conserved in guinea pig.";  
RL J. Immunol. 151:6225-6236(1993).  
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS, BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXCL).

CC -----  
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CC -----

CC EMBL; L04986; AAA37049.1; -;  
DR HSSP; P10145; 21L8.  
DR InterPro: IPR001089; CXCL\_Chmkine\_sm1.  
DR InterPro: IPR001811; Chemokine\_IL8.  
DR Pfam: PF00048; IL8; 1.  
DR PRINTS; PR00437; SMALLCYTRKCXC.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00471; SMALL\_CYTOKINES\_CXC; 1.  
KW CYTOKINE; Chemotaxis; Inflammatory response; Signal.  
FT SIGNAL 1 22 BY SIMILARITY.  
FT CHAIN 23 101 INTERLEUKIN-8.  
FT DISULFID 34 61 BY SIMILARITY.  
FT DISULFID 36 77 BY SIMILARITY.  
SQ SEQUENCE 101 AA; 11414 MW; 557E2A9E15F6727F CRC64;

Query Match 28.1%; Score 101; DB 1; Length 101;  
Best Local Similarity 35.9%; Pred. No. 1.4e-05;  
Matches 23; Conservative 16; Mismatches 17; Indels 8; Gaps 5;

OY 8 RCPREFESHVARAN---VKHLKILNT--PNCA-LOIVARLKNNNROVCIDPKLKW 62  
DB 33 RCOC--IKHTSPFPFKIKELRLVIDSGPHCENSEITIVKL--SDNRKCLDPKRWQDVV 89

OY 63 EKAL 66  
DB 90 SMFL 93

RESULT 6  
IL8\_FELCA ID IL8\_FELCA STANDARD; PRT; 101 AA.

AC Q9XSX5;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Interleukin-8 precursor (IL-8) (CXCL8).  
GN Felis silvestris catus (Cat).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
ON NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Straubinger A.F., Simpson K.W., Straubinger R.K.;  
RT "Feline interleukin-8 mRNA.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS, BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXCL).

CC -----  
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CC -----

CC EMBL; AF158598; AAD40323.1; -;  
DR HSSP; P10145; 1IKM.  
DR InterPro: IPR001089; CXCL\_Chmkine\_sm1.  
DR InterPro: IPR001811; Chemokine\_IL8.  
DR Pfam: PF00048; IL8; 1.  
DR PRINTS; PR00437; SMALLCYTRKCXC.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00471; SMALL\_CYTOKINES\_CXC; 1.  
KW CYTOKINE; Chemotaxis; Inflammatory response; Signal.  
FT SIGNAL 1 22 BY SIMILARITY.  
FT CHAIN 23 101 INTERLEUKIN-8.  
FT DISULFID 34 61 BY SIMILARITY.  
FT DISULFID 36 77 BY SIMILARITY.  
SQ SEQUENCE 101 AA; 11165 MW; 690D97F13EF79120 CRC64;

Query Match 27.3%; Score 98; DB 1; Length 101;  
Best Local Similarity 33.3%; Pred. No. 3.2e-05;  
Matches 22; Conservative 18; Mismatches 18; Indels 8; Gaps 5;

OY 3 VSLSYRCPREFESHVARAN---VKHLKILNT--PNCA-LOIVARLKNNNROVCIDPKLKW 57  
DB 28 ISSLRQC--IKHTSPFPFKIKELRLVIDSGPHCENSEITIVKL--NGKEVCIDPKRKM 84

OY 58 IOEYLE 63  
DB 85 VQKVE 90

RESULT 7  
IL8\_HUMAN ID IL8\_HUMAN STANDARD; PRT; 99 AA.

AC P10145; Q9C077; Q96RG6;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-8 precursor (IL-8) (CXCL8) (Monocyte-derived neutrophil  
 DE chemotactic factor) (MDMCF) (T-cell chemotactic factor) (Neutrophil-  
 DE activating protein 1) (NAP-1) (Lymphocyte-derived neutrophil-  
 DE activating factor) (LYNAP) (Protein 3-10C) (Neutrophil-activating  
 DE factor) (NAF) (Granulocyte chemotactic protein 1) (GCP-1) (Emoctrakin).  
 GN IL8.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxId:9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=88258376; PubMed=3260265;  
 RA Matsushima K., Morishita K., Yoshimura T., Lavi S., Kobayashi Y.,  
 RA Lew W., Appella E., Kung H., Leonard E.J., Oppenheim J.J.;  
 RT "Molecular cloning of a human monocyte-derived neutrophil chemotactic  
 RT factor (MDMCF) and the induction of MDMCF mRNA by interleukin 1 and  
 RT tumor necrosis factor.";  
 RL J. Exp. Med. 167:1883-1893(1988).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=87224164; PubMed=2953813;  
 RA Schmid J., Weismann C.;  
 RT "Induction of mRNA for a serine protease and a  
 RT beta-thromboglobulin-like protein in mitogen-stimulated human  
 RT leukocytes.";  
 RL J. Immunol. 139:250-256(1987).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=89313739; PubMed=2664463;  
 RA Kowalski J., Denhardt D.T.;  
 RT "Regulation of the mRNA for monocyte-derived neutrophil-activating  
 RT peptide in differentiating HL60 promyelocytes.";  
 RL Mol. Cell. Biol. 9:1946-1957(1989).  
 RN [4]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=89309826; PubMed=2663993;  
 RA Mukaida N., Shitro M., Matsushima K.;  
 RT "Genomic structure of the human monocyte-derived neutrophil  
 RT chemotactic factor IL-8.";  
 RL J. Immunol. 143:1366-1371(1989).  
 RN [5]  
 RN SEQUENCE FROM N.A.  
 RA Ishikawa J.;  
 RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RN SEQUENCE FROM N.A. (ISOFORM 2).  
 RA Jang J.S., Kim B.E.;  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RN SEQUENCE FROM N.A.  
 RA Rieder M.J., Carlington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
 RA Nickerson D.A.;  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RN SEQUENCE OF 23-46.  
 RX MEDLINE=89246368; PubMed=2655583;  
 RA Golds E.E., Mason P., Nytkos P.;  
 RT "Inflammatory cytokines induce synthesis and secretion of gro protein  
 RT and a neutrophil chemotactic factor but not beta 2-microglobulin in  
 RT human synovial cells and fibroblasts.";  
 RL Biochem. J. 259:585-588(1989).  
 RN [9]  
 RN SEQUENCE OF 23-54.  
 RX MEDLINE=89279141; PubMed=2659722;  
 RA Suzuki K., Miyasaka H., Ota H., Yamakawa Y., Tagawa M., Kuramoto A.,  
 RA Mizuno S.;  
 RT "Purification and partial primary sequence of a chemotactic protein  
 RT for polymorphonuclear leukocytes derived from human lung giant cell  
 RT carcinoma LU66C cells.";  
 RL J. Exp. Med. 169:1895-1901(1989).  
 RN [10]  
 RN SEQUENCE OF 28-99.  
 RX MEDLINE=88162914; PubMed=3279957;  
 RA Gregory H., Young J., Schroeder J.M., Mrowietz U., Christophers E.;  
 RT "Structure determination of a human lymphocyte derived neutrophil  
 RT activating peptide (LYNAP).";  
 RL Biochem. Biophys. Res. Commun. 151:883-890(1988).  
 RN [11]  
 RN SEQUENCE OF 28-59.  
 RX MEDLINE=88106502; PubMed=3322281;  
 RA Walz A., Feveri P., Aschauer H., Baggiolini M.;  
 RT "Purification and amino acid sequencing of NAF, a novel neutrophil-  
 RT activating factor produced by monocytes.";  
 RL Biochem. Biophys. Res. Commun. 149:755-761(1987).  
 RN [12]  
 RN SEQUENCE OF 28-69.  
 RX MEDLINE=88097462; PubMed=3480540;  
 RA Yoshimura T., Matsushima K., Tanaka S., Robinson E.A., Appella E.,  
 RA Oppenheim J.J., Leonard E.J.;  
 RT "Purification of a human monocyte-derived neutrophil chemotactic  
 RT factor that has peptide sequence similarity to other host defense  
 RT cytokines.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:9233-9237(1987).  
 RN [13]  
 RN N-TERMINAL FORMS.  
 RX MEDLINE=91006326; PubMed=2145175;  
 RA van Damme J., Rampart M., Conling R., Decock B., van Osselaer N.,  
 RA Willems J., Billiau A.;  
 RT "The neutrophil-activating proteins interleukin 8 and beta-  
 RT thromboglobulin: in vitro and in vivo comparison of NH2-terminally  
 RT processed forms.";  
 RL Eur. J. Immunol. 20:2113-2118(1990).  
 RN [14]  
 RN N-TERMINAL FORMS.  
 RX MEDLINE=89231715; PubMed=2523801;  
 RA van Damme J., van Beeumen J., Conings R., Decock B., Billiau A.;  
 RT "Purification of granulocyte chemotactic peptide/interleukin-8  
 RT reveals N-terminal sequence heterogeneity similar to that of  
 RT beta-thromboglobulin.";  
 RL Eur. J. Biochem. 181:337-344(1989).  
 RN [15]  
 RN SYNTHESIS OF 28-99.  
 RX MEDLINE=91175767; PubMed=2007144;  
 RA Clark-Lewis I., Mose B., Walz A., Baggiolini M., Scott G.J.,  
 RA Aebersold R.;  
 RT "Chemical synthesis, purification, and characterization of two  
 RT inflammatory proteins, neutrophil activating peptide 1  
 RT (interleukin-8) and neutrophil activating peptide.";  
 RL Biochemistry 30:3128-3135(1991).  
 RN [16]  
 RN REVIEW.  
 RX MEDLINE=92347562; PubMed=1639201;  
 RA Baggiolini M., Clark-Lewis I.;  
 RT "Interleukin-8, a chemotactic and inflammatory cytokine.";  
 RL FEBS Lett. 307:97-101(1992).  
 RN [17]  
 RN STRUCTURE BY NMR.  
 RX MEDLINE=90234679; PubMed=2184886;  
 RA Clore G.M., Appella E., Yamada M., Matsushima K., Gronenborn A.M.;  
 RT "Three-dimensional structure of Interleukin 8 in solution.";  
 RL Biochemistry 29:1689-1696(1990).  
 RN [18]  
 RN STRUCTURE BY NMR OF COMPLEX TO RECEPTOR.  
 RX MEDLINE=99148123; PubMed=10368283;  
 RA Skelton N.J., Quan C., Reilly D., Lowman H.;  
 RT "Structure of a CXCR chemokine-receptor fragment in complex with  
 RT interleukin-8.";  
 RL Structure 7:157-168(1999).  
 RN [19]  
 RN X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 RX MEDLINE=90216714; PubMed=2182630;  
 RA Baldwin E.T., Franklin K.A., Appella E., Yamada M., Matsushima K.,  
 RA Wlodawer A., Weber I.T.;  
 RT "Crystallization of human interleukin-8. A protein chemotactic for

```

RT  neutrophils and T-lymphocytes." ;
RL  J. Biol. Chem. 265:6851-6853(1990).
RN
RN  (20)
RX  X-RAY CRYSTALLOGRAPHY, AND STRUCTURE BY NMR.
RX  MEDLINE=91171286; PubMed=2005614;
RA  Clore G.M., Gronenborn A.M.;
RT  "Comparison of the solution nuclear magnetic resonance and crystal
RT  structures of interleukin-8. Possible implications for the mechanism
RT  of receptor binding." ;
RL  J. Mol. Biol. 217:611-620(1991).
RN
RN  (21)
RX  X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS), AND STRUCTURE BY NMR.
RX  MEDLINE=91110556; PubMed=198949;
RA  Baldwin E.T., Weber I.T., St Charles R., Xuan J.C., Appella E.,
RA  Yamada M., Matsushima K., Edwards B.F., Clore G.M., Gronenborn A.M.;
RT  "Crystal structure of interleukin 8: symbiosis of NMR and
RT  crystallography" ;
RL  Proc. Natl. Acad. Sci. U.S.A. 88:502-506(1991).
RN
RN  (22)
RX  X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF MUTANT.
RX  MEDLINE=20178334; PubMed=10707023;
RA  Geder N., Lowman H., Artis D.R., Eigenbrodt C.;
RT  "Receptor-binding conformation of the 'ELR' motif of IL-8: X-ray
RT  structure of the L5C/H33C variant at 2.35 A resolution." ;
RL  Proteins 38:361-367(2000).
CC  -I- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC  BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC  NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC  RESPONSE TO AN INFLAMMATORY STIMULUS.
CC  -I- SUBUNIT: HOMODIMER.
CC  -I- SIMILARITY: BELONGS TO THE INTERFERIN ALPHA FAMILY (SMALL CYTOKINE
CC  C-X-C) (CHEMOKINE CXC).
CC
CC  -----
CC  CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  CC  or send an email to license@isb-sib.ch).
CC  CC
DR  EMBL: Y00787; CA68742.1; -
DR  EMBL: M17017; AAA35611.1; -
DR  EMBL: M26383; AAA36323.1; -
DR  EMBL: M28130; AAA59158.1; -
DR  EMBL: D14283; BAA03245.1; -
DR  EMBL: AF043337; AAK00048.1; -
DR  EMBL: AF385628; AAK60276.1; ALT_SEQ.
DR  PIR: A37034; A37034.
DR  PIR: S03975; S03975.
Query Match 26.2%; Score 94; DB 1; Length 99;
Best Local Similarity 32.3%; Pred.No. 9.5e-05;
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;
OY  8 KCPG-RFESHVARANVXKILNTN-PNCA-LQIYARLKNNRQVCIDPKLWIDYLEK 64
DB  33 RQCIKITYSKRPHKFIKELRVIESGPHCANTEIIYKL-SDGRELDCLPKENWVORVEK 91
OY  65 AL 66
DB  92 FL 93
RESULT 8
IL8_SHEEP
ID  IL8_SHEEP STANDARD; PRT; 101 AA.
AC  P36925;
DT  01-JUN-1994 (Rel. 29, Created)
DT  01-JUN-1994 (Rel. 29, Last sequence update)
DE  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Interleukin-8 precursor (IL-8) (CXCL8).
GN  IL8.

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OS Ovis aries (Sheep).
CC Exkaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
CC Bovidae; Caprinae; Ovis.
OX NCBI_taxid:9940;
RN [1]
RP
RX SEQUENCE FROM N.A.
MEDLINE:95121933; PubMed:7821808;
RA Legastelots I., Greenland T., Arraud P., Mornex J.F., Cordier G.;
RT "Sequencing of the ovine Interleukin-8-encoding cDNA using the
RT polymerase chain reaction.";
RL Gene 150:367-369(1994).
RN [2]
RP
RX SEQUENCE FROM N.A.
MEDLINE:95137691; PubMed:7835984;
RA Seow H.F., Yoshimura T., Wood P.R., Colditz I.G.;
RT "Cloning, sequencing, expression and inflammatory activity in skin of
RL ovine interleukin-8.";
RL Immunol. Cell Biol. 72:398-405(1994)
CC
CC -!- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SIMILARITY: BELONGS TO THE INTERFERIN ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
CC -----
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CC -----
DR EMBL: X78306; CAA55115.1; -.
DR EMBL: S74436; AAB33241.1; -.
DR PIR: S42496; S42496.
DR HSSP: P10145; 1IKM.
DR InterPro: IPR001089; CXC_chmkline_sm11.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8: 1.
DR PRINTS: PR00437; SMALLCYTCKXC.
DR SMART: SM00199; SCY.1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cyclokin; Chemotaxis; Inflammatory response; signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 101 INTERLEUKIN-8.
FT DISULFD 34 61 BY SIMILARITY.
FT DISULFD 36 77 BY SIMILARITY.
SQ SEQUENCE 101 AA; 11292 MW; 40EB841B57C56A5B CRC64;

Query Match 25.9%; Score 93; DB 1; Length 101;
Best Local Similarity 30.4%; Pred. No. 0.00013;
Matches 21; Conservative 20; Mismatches 20; Indels 8; Gaps 5;

OY 3 VSLSTRCPCREFESHAVARAN--VKHLKILNT-PNCA-LQIVARKNNRQYCIDPKLKW 57
   1 11 1 : : 1 : : 1 : : 1 : : 1 : : 1 : : 1 : : 1 : : 1 : : 1
DB 28 MSTELRCQC--IKTSTPFHPEFKELRVIESGPCENSEIIVKL-TWGKEVCIDPKKEKW 84
   1 1 1 : : 1 : : 1 : : 1 : : 1 : : 1 : : 1 : : 1 : : 1 : : 1

OY 58 IOEYLEKAL 66
   1 : : 1 : : 1 : : 1 : : 1 : : 1 : : 1 : : 1 : : 1 : : 1 : : 1

DB 85 VQKVQAFEL 93
   1 : : 1 : : 1 : : 1 : : 1 : : 1 : : 1 : : 1 : : 1 : : 1 : : 1

RESULT 9
ID IL8_PIG STANDARD; PRT; 103 AA.
AC P26894; P22951;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-JUN-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8) (Alveolar macrophage

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DE chemotactic factor I) (AMCF-I).  
GN IL8.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxId=9823;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA Lin G., Pearson A.E., Scamurra R.W., Zhou Y., Baarsch M.J.,  
RA Weiss D.J., Murtough M.P.;  
RT "Regulation of Interleukin-8 expression in porcine alveolar  
RT macrophages by bacterial lipopolysaccharide.";  
RL J. Biol. Chem. 269:77-85(1994).  
RN (2)  
RP SEQUENCE FROM N.A.  
RA Sanjanvala M.;  
RL Submitted (JUL-1991) to the EMBL/Genbank/DBJ databases.  
RN (3)  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 26-45.  
RC TISSUE=Lung;  
RX MEDLINE=93041741; PubMed=8276881;  
RA Goodman R.B., Foster D.C., Mathews S.L., Osborn S.G., Kijper J.L.,  
RA Forstrom J.W., Martin T.R.;  
RT "Molecular cloning of porcine alveolar macrophage-derived neutrophil  
RT chemotactic factors I and II: Identification of porcine IL-8 and  
RT another interleukin-alpha protein.";  
RL Biochemistry 31:10483-10490(1992).  
RN (4)  
RP REVISION TO 23.  
RA Goodman R.B.;  
RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.  
RN (5)  
RP SEQUENCE OF 26-45.  
RC STRAIN=Yorkshire;  
RX MEDLINE=91217086; PubMed=1850745;  
RA Goodman R.B., Forstrom J.W., Osborn S.G., Chi E.Y., Martin T.R.;  
RT "Identification of two neutrophil chemotactic peptides produced by  
RT porcine alveolar macrophages.";  
RL J. Biol. Chem. 266:8455-8463(1991).  
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,  
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN  
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN  
CC RESPONSE TO AN INFLAMMATORY STIMULUS.  
CC -1- SUBUNIT: HOMODIMER.  
CC -1- TISSUE SPECIFICITY: ALVEOLAR MACROPHAGES.  
CC -1- INDUCTION: BY LIPOPOLYSACCHARIDE (LPS).  
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE  
CC C-X-C) (CHEMOKINE CXC).  
CC -----  
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CC -----  
CC EMBL: M86923; AAA16616.1;  
CC EMBL: X61151; CAA43461.1;  
CC EMBL: M99367; AAA92576.1;  
CC PIR: A44253; A44253.  
CC PIR: A39819; A39819.  
CC HSP: P10145; 1IKM.  
CC InterPro: IPR001089; CXC\_cxmkline\_sm11.  
CC InterPro: IPR001811; Chemokine\_IL8.  
CC Pfam: PF00048; IL8; 1.  
CC PRINTS: PR00437; SMALLCYTKCXC.  
CC SMART: SMD0199; SCY, 1.  
CC PROSITE: PS00471; SMALL\_CYTOKINES\_CXC, 1.  
CC Cytokine; Chemotaxis; Inflammatory response; Signal.  
CC SIGNAL 1 25  
CC CHAIN 26 103 INTERLEUKIN-8.

FT DISULFID 34 61 BY SIMILARITY.  
FT DISULFID 36 77 BY SIMILARITY.  
FT CONFLICT 33 34 RC -> CR (IN REF. 5).  
FT CONFLICT 87 87 K -> KK (IN REF. 2).  
SQ SEQUENCE 103 AA; 11633 MM; 9FE0E350E1928C64 CRC64;  
Query Match 25.6%; Score 92; DB 1; Length 103;  
Best Local Similarity 31.8%; Pred. No. 0.00017;  
Matches 21; Conservative 18; Mismatches 19; Indels 8; Gaps 5;  
OY 3 VSLSTRPCRFESHVARN---VKKLTLNT-PNCA-LQIYARLKNNRNVCIDPKLW 57  
DB 28 VAEILRCQC--INTNSTPFPKFIKELRVIESGPHCENSEIIVKLIV-NCKEYCLDPKRW 84  
OY 58 IOEYLE 63  
DB 85 VQKVQV 90  
RESULT 10  
GRO\_MOUSE  
ID GRO\_MOUSE STANDARD; PRT: 96 AA.  
AC P12850;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Growth regulated protein precursor (CXCL) (Platelet-derived growth  
DE factor-induced protein KC) (Secretory protein NS1).  
GN SCYB1 OR GRO1 OR GRO OR MGS4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89139485; PubMed=2917992;  
RA Oquendo P., Alberta J., Wen D., Graycar J.L., Derynck R., Stiles C.D.;  
RT "The platelet-derived growth factor-inducible KC gene encodes a  
RT secretory protein related to platelet alpha-granule proteins.";  
RL J. Biol. Chem. 264:4133-4137(1989).  
RN (2)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89078502; PubMed=2909392;  
RA Ryseck R.P., Macdonald-Bravo H., Matrei M.-G., Bravo R.;  
RT "Cloning and sequence of a secretory protein induced by growth  
RT factors in mouse fibroblasts.";  
RL Exp. Cell Res. 180:266-275(1989).  
RN (3)  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/Sv.  
RA Bozic C.R., Kolakowski L.F. Jr., von Uexkull C., Garcia-Rodriguez M.,  
RA Conklin M.J., Breslow R., Showell H.J., Gerard N.P., Gerard C.;  
RL Submitted (FEB-1995) to the EMBL/Genbank/DBJ databases.  
RN (4)  
RP SEQUENCE OF 1-10 FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=96016008; PubMed=7561058;  
RA Ohmori Y., Fukumoto S., Hamilton T.A.;  
RT "Two structurally distinct kappa B sequence motifs cooperatively  
RT control LPS-induced KC gene transcription in mouse macrophages.";  
RL J. Immunol. 155:3593-3600(1995).  
CC -1- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. CONTRIBUTES TO  
CC NEUTROPHIL ACTIVATION DURING INFLAMMATION (BY SIMILARITY).  
CC -1- INDUCTION: BY PLATELET-DERIVED GROWTH FACTOR. IN LUNG, BY  
CC LIPOPOLYSACCHARIDE OR INFLAMMATION (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE  
CC C-X-C) (CHEMOKINE CXC).  
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CC -----

DR EMBL: J04596; AAA0131.1; -

DR EMBL: U20634; AAB03376.1; -

DR EMBL: U20524; AAB03376.1; JOINED.

DR EMBL: S79767; -; NOT\_ANNOTATED\_CDS.

DR PIR: A32954; A32954.

DR PIR: JH0081; JH0081.

DR HSP: P19875; 10NK.

DR MGD: MGI:108068; Gc01.

DR InterPro: IPR001089; CXC\_chmkine\_sm11.

DR InterPro: IPR001811; Chemokine\_IL8.

DR Pfam: PF00048; IL8; 1.

DR PRINTS: PR00437; SMALLCYTRKCXC.

DR SMART: SM00199; SCY; 1.

DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; 1.

DR CytoKine: Growth factor; Inflammatory response; Signal.

FT SIGNAL 1 24 PROBABLE.

FT CHAIN 25 96 GROWTH REGULATED PROTEIN.

FT DISULFID 33 59 BY SIMILARITY.

FT DISULFID 35 75 BY SIMILARITY.

SO SEQUENCE 96 AA; 10254 MW; 4A52B5E5C3845C2 CRC64;

Query Match 25.5%; Score 91.5; DB 1; Length 96;

Best Local Similarity 32.8%; Pred. No. 0.00019;

Matches 20; Conservative 17; Mismatches 21; Indels 3; Gaps 3;

Qy 8 RCPCRFESHVAVRANVHKIL-NTFPCA-LQIVARLKNNRQVCTDPKLTQIOEYLEKA 65

Db 32 RCQCLQTMAGIHLKNIQSLKVLPSGPHCTQTEVIATLK-NGREACLDPEAPLVQKIVOKM 90

Qy 66 L 66

Db 91 L 91

RESULT 11

IL8\_MACMU

ID IL8\_MACMU STANDARD; PRT; 101 AA.

AC P51495;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Interleukin-8 precursor (IL-8) (CXCL8).

GN IL8.

OS Macaca mulatta (Rhesus macaque), and

OS Macaca nemestrina (Pig-tailed macaque).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Macaca.

OX NCBI\_TaxID=9544, 9545;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Blood;

RC MEDLINE=96003435; PubMed=7561102;

RA Villinger F.J., Brar S.S., Mayne A.E., Chikala N., Ansari A.A.;

RT "Comparative sequence analysis of cytokine genes from human and nonhuman primates."

RT J. Immunol. 153:3946-3954(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC SPECIES=M.mulatta; TISSUE=Blood;

RC MEDLINE=9535137; PubMed=7628861;

RA Minerley J.C., Baganoff M.P., Deppeler C.L., Keller B.T.,

RA Rapp S.R., Wlowski D.L., Fretland D.J., Bolanowski M.A.;

RT "Identification and characterization of rhesus macaque interleukin-8."

RT Interleukin-8."

RL Inflammation 19:313-331(1995).

CC -I- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS, BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).

CC -I- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -I- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXC).

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CC -----

DR EMBL: U19849; AAA86711.1; -

DR EMBL: U19851; AAA86713.1; -

DR EMBL: S78555; AAA80141.2; -

DR HSP: P10145; 2IL8.

DR InterPro: IPR001089; CXC\_chmkine\_sm11.

DR InterPro: IPR001811; Chemokine\_IL8.

DR Pfam: PF00048; IL8; 1.

DR PRINTS: PR00437; SMALLCYTRKCXC.

DR SMART: SM00199; SCY; 1.

DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; 1.

DR CytoKine: Chemotaxis; Inflammatory response; Signal.

FT SIGNAL 1 22 BY SIMILARITY.

FT CHAIN 23 101 INTERLEUKIN-8.

FT DISULFID 34 61 BY SIMILARITY.

FT DISULFID 36 77 BY SIMILARITY.

SO SEQUENCE 101 AA; 11320 MW; 42BCF9C97C84B5F9 CRC64;

Query Match 25.3%; Score 91; DB 1; Length 101;

Best Local Similarity 31.7%; Pred. No. 0.00023;

Matches 19; Conservative 18; Mismatches 19; Indels 4; Gaps 4;

Qy 8 RCPCRFESHVAVRANVHKILNT-PNCA-LQIVARLKNNRQVCTDPKLTQIOEYLEKA 64

Db 33 RCBCIKTYSPFHPKFKLELVIESGPHCANETITVVL-SDGRCLDPEAPVQRYVER 91

RESULT 12

SY05\_MOUSE

ID SY05\_MOUSE STANDARD; PRT; 91 AA.

AC P30882;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Small inducible cytokine A5 precursor (CCl5) (T-cell specific RANTES protein) (SIS-delta) (Murantes).

DE SCYAS.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=92277990; PubMed=1375672;

RA Heeger P., Wolf G., Meyers C., Sun M.J., O'Farrell S.C.,

RA Krensky A.M., Nelson E.G.;

RT "Isolation and characterization of cDNA from renal tubular epithelium encoding murine Rantes."

RT Kidney Int. 41:220-225(1992).

RN [2]

RP SEQUENCE FROM N.A.

RC MEDLINE=92289805; PubMed=1376260;

RA Schall T.J., Simpson N.J., Mak J.Y.;

RT "Molecular cloning and expression of the murine RANTES cytokine: structural and functional conservation between mouse and man."

RT Eur. J. Immunol. 22:1477-1481(1992).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=NIH Swiss;

RC MEDLINE=94132613; PubMed=7507961;

RA Danoff T.M., Talley P.A., Chang Y.S., Heeger P.S., Nelson E.G.;

RT "Cloning, genomic organization, and chromosomal localization of the

```

RT scya5 gene encoding the murine chemokine RANTES."
RL J. Immunol. 152:1182-1189(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/c:
RX MEDLINE-94217689; PubMed-7513046;
RA Shln H.S., Drysdale B.E., Shln M.L., Noble P.W., Fisher S.N.,
RA Paznekas W.A.:
RT "Definition of a lipopolysaccharide-responsive element in the 5'-
RL flanking regions of Murantes and crg-2."
RL Mol. Cell. Biol. 14:2914-2925(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/cJ.B10.S/J, NOD/LtJ, and SJL/J; TISSUE-Spleen;
RA Ma R.Z., Teuscher C.:
RL Submitted (Mar-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
CC BASOPHILS AND ACTIVATES EOSINOPHILS.
CC -1- TISSUE SPECIFICITY: T-CELL AND MACROPHAGE SPECIFIC.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
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-----
DR EMBL: M7747; AAA0029.1; -
DR EMBL: S7648; AAB2230.1; -
DR EMBL: U02298; AAI18302.1; -
DR EMBL: X70675; CA55001.1; -
DR EMBL: AF065944; AAC17511.1; -
DR EMBL: AF065945; AAC17512.1; -
DR EMBL: AF065946; AAC17513.1; -
DR EMBL: AF065947; AAC17514.1; -
DR HSSP: P13501; 1RTN.
DR MGI: 98262; SCYA5.
DR InterPro: IPR000827; CC_chemkine.sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.
FT SIGNAL 1 23
FT CHAIN 24 91
FT DISULFID 33 57
FT DISULFID 34 73
FT DISULFID 19 19
FT CONFLICT 41 41
FT CONFLICT 41 41
SQ SEQUENCE 91 AA; 10071 MW; 5DP66F4684FE1C8 CRC64;

Query Match 25.2%; Score 90.5; DB 1; Length 91;
Best local Similarity 38.2%; Pred. No. 0.00023;
Matches 21; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

Db 10 PCFFESHVA--RANKHLKILTPNCALQIVARLKNNNRQVCIDPKLKWIOEYL 62
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33 PCFFAVLSLALPRAHKEY-FYTSSKCSNLAVFVTRRRQVCANPEKKWQVEYI 85
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33 PCFFAVLSLALPRAHKEY-FYTSSKCSNLAVFVTRRRQVCANPEKKWQVEYI 85

RESULT 13
SY05_RAT STANDARD: PRT: 92 AA.
AC P50231;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES

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DE protein) (SIS-delta).
GN SCYA5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-long Evans; TISSUE-Lung;
RA Jones M.L., Shanley T.P., Ward P.A.:
RL Submitted (Feb-1994) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
CC BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
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CC or send an email to license@sib-sib.ch).
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DR EMBL: U06436; AAA96499.1; -
DR HSSP: P13501; 1RTN.
DR InterPro: IPR000827; CC_chemkine.sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.
FT SIGNAL 1 24
FT CHAIN 25 92
FT DISULFID 34 58
FT DISULFID 35 74
FT DISULFID 35 74
SQ SEQUENCE 92 AA; 10170 MW; B4FBC2B4208A8C6 CRC64;

Query Match 25.2%; Score 90.5; DB 1; Length 92;
Best local Similarity 38.2%; Pred. No. 0.00024;
Matches 21; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

Db 10 PCFFESHVA--RANKHLKILTPNCALQIVARLKNNNRQVCIDPKLKWIOEYL 62
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33 PCFFAVLSLALPRAHKEY-FYTSSKCSNLAVFVTRRRQVCANPEKKWQVEYI 86
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33 PCFFAVLSLALPRAHKEY-FYTSSKCSNLAVFVTRRRQVCANPEKKWQVEYI 86

RESULT 14
IL8_BOVIN STANDARD: PRT: 101 AA.
AC P79255;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN IL8.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE-96304552; PubMed-8737490;
RA Morsey M.A., Popowycz Y., Kowalski J., Gerlach G., Godson D.,
RA Campos M., Babiuk L.A.:
RT "Molecular cloning and expression of bovine interleukin-8."
RL Microb. Pathog. 20:203-212(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Galligan C.L., Yoshimura T., Coomber B.L.:

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RT "Cloning and sequencing of bovine Interleukin 8 cDNA isolated from
RT 1lipopolysaccharide stimulated monocytes in vitro."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXCL).
CC -----
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CC -----
CC EMBL; S82598; AAB37483.1; -.
DR EMBL; AF232704; AAF37575.1; -.
DR HSSP; P10145; 1IKM.
DR InterPro; IPR001089; CXCL; chemokine_sml1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTKCX.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Chemotaxis; Inflammatory response; Signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 101 INTERLEUKIN-8.
FT DISULFID 34 61 BY SIMILARITY.
FT DISULFID 36 77 BY SIMILARITY.
SQ SEQUENCE 101 AA; 11291 MW; 061A530507906736 CRC64;

Query Match 25.1%; Score 90; DB 1; Length 101;
Best Local Similarity 30.3%; Pred. No. 0.0003;
Matches 20; Conservative 20; Mismatches 18; Indels 8; Gaps 5;

OY 3 VSLSYRCPCRFESHVARAN---VKHLKIILNT-PNCA-LOIIVARLKNNNROYCIDPKLKW 57
DB 28 MSTELRCOC--IKTHSPFPKFKELKRVESGPHCENSEITIVKLTNGN-EVCLNPKKRW 84
OY 58 IOEYLE 63
DB 85 VQKVVQ 90

RESULT 15
SZ05_RAT STANDARD; PRT; 130 AA.
ID SZ05_RAT
AC P97885;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine B5 precursor (CXCL5) (Cytokine LIX).
GN SCYB5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RA Keiner G.S.; Maciejewski-Lenoir D.; Lee E.D.; Maki R.A.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAY PARTICIPATE IN THE RECRUITMENT OF INFLAMMATORY CELLS
CC BY INJURED OR INFECTED TISSUE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXCL).
CC -----
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CC -----
CC EMBL; U90448; AAB61460.1; -.
DR EMBL; P10889; 1MI2.
DR InterPro; IPR001089; CXCL; chemokine_sml1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTKCX.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Signal.
FT SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 130 SMALL INDUCIBLE CYTOKINE B5.
FT DISULFID 50 76 BY SIMILARITY.
FT DISULFID 52 93 BY SIMILARITY.
SQ SEQUENCE 130 AA; 14263 MW; C00F6B3605524F4E CRC64;

Query Match 25.1%; Score 90; DB 1; Length 130;
Best Local Similarity 27.3%; Pred. No. 0.00039;
Matches 18; Conservative 19; Mismatches 27; Indels 2; Gaps 2;

OY 3 VSLSYRCPCRFESHVARANVKHLKIILNT-PNCA-LOIIVARLKNNNROYCIDPKLKW 60
DB 44 VATELRVCCLTLNAPRIKMIANLEVIAPGPHCPKVEIVAKLNQNDVCLDQAPLIKK 103
OY 61 YLEKAL 66
DB 104 VIOKIL 109

Search completed: January 23, 2003, 15:34:18
Job time : 7 secs

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RESULT 2  
 Q9QZD1 PRELIMINARY; PRT; 89 AA.  
 AC Q9QZD1;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE Stromal cell-derived factor-1 alpha.  
 GN SDF-1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RA Ohtani Y., Okada M., Kawaguchi N., Minami M., Satoh M.;  
 RT "cDNA cloning of rat stromal cell-derived factor-1 alpha (SDF-1  
 RT alpha).";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Pillariseti K., Gupta S.K.;  
 RT "Identification and molecular cloning of a novel rat ortholog of the  
 RT alpha chemokine, stromal cell derived factor-1 (SDF-1).";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF189724; AAF01066.1; -;  
 DR EMBL; AF209976; AAC43506.1; -;  
 DR HSSP; P48061; 1SDF.  
 DR Interpro: IPR001811; Chemokine\_IL8.  
 DR Pfam; PF00048; IL8; 1.  
 DR SMART; SM00199; SCY; 1.  
 SQ SEQUENCE 89 AA; 9977 MW; D86977626A2E35FA CRC64;

Query Match 95.5%; Score 343; DB 11; Length 89;  
 Best Local Similarity 95.5%; Pred. No. 4.8e-35;  
 Matches 64; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 KGVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60  
 DB 22 KPVSLSTRCPREFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 81  
 OY 61 YLEKALN 67  
 DB 82 YLDKALN 88

RESULT 3  
 Q8UUG9 PRELIMINARY; PRT; 94 AA.  
 AC Q8UUG9;  
 DT 01-MAR-2002 (Tremblrel. 20, Created)  
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Stromal-derived factor 1 precursor.  
 GN SDF-1.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesodactylia; Pipidea; Pipidae;  
 OC Xenopodidae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SPLEEN;  
 RA Braun M., Wunderlin M., Knoechel W., Giersch P., Moepfs B.;  
 RT "Xenopus laevis stromal-derived factor 1: conservation of structure  
 RT and function during vertebrate development.";  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; A1778857; CAC82196.1; -;  
 DR Interpro: IPR001811; Chemokine\_IL8.  
 DR Pfam; PF00048; IL8; 1.  
 DR SMART; SM00199; SCY; 1.  
 KW Signal.

FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 94 STROMAL-DERIVED FACTOR 1.  
 SQ SEQUENCE 94 AA; 10701 MW; 8C8325D152F326E7 CRC64;

Query Match 79.4%; Score 285; DB 13; Length 94;  
 Best Local Similarity 74.6%; Pred. No. 7.9e-28;  
 Matches 50; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

OY 1 KGVSLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60  
 DB 22 KPVSLSTRCPREFESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 81  
 OY 61 YLEKALN 67  
 DB 82 YLEKALN 88

RESULT 4  
 Q91ZL1 PRELIMINARY; PRT; 91 AA.  
 AC Q91ZL1;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE RANTES chemokine.  
 OS Sigmodon hispidus (Hispid cotton rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 OC Sigmodon.  
 OX NCBI\_TaxID=42415;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bianco J.C., Pietreva L.M., Prince G.A.;  
 RT "Stimodon hispidus cytokines, chemokines and interferons.";  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF421391; AAL16932.1; -;  
 DR Interpro: IPR000827; CC\_chemkine\_sm1.  
 DR Interpro: IPR001811; Chemokine\_IL8.  
 DR Pfam; PF00048; IL8; 1.  
 DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; UNKNOWN.1.  
 SQ SEQUENCE 91 AA; 10082 MW; DDD6EAEABE4242FF CRC64;

Query Match 26.0%; Score 93.5; DB 11; Length 91;  
 Best Local Similarity 38.2%; Pred. No. 0.00044;  
 Matches 21; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

OY 10 PCRF--FESHVARANVHKILNTPNCALQIVARLKNNNQVCIDPKLKWIOEYL 62  
 DB 32 PCCFAYLAVLPRAHVKEX-FYTSSKCSNFAVYVFRNRQVCANPKKWOEYI 85

RESULT 5  
 Q8QGV8 PRELIMINARY; PRT; 98 AA.  
 AC Q8QGV8;  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE CXCL chemokine.  
 GN CXCL CHEMOKINE.  
 OS Paralicthys olivaceus (Flounder).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
 OC Pleuronectoidae; Paralicthysidae; Paralicthys.  
 OX NCBI\_TaxID=8255;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Aoki T., Hirano I., Lee J., Iwahori A.;  
 RT "Molecular cloning and expression of IL-1b and two types of chemokines  
 RT in Japanese flounder, Paralicthys olivaceus.";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB070837; BAB86884.1; -;

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SQ SEQUENCE 98 AA: 10846 MW: 495CA4839A5D8C92 CRC64;
Query Match 24.5%; Score 88; DB 13; Length 98;
Best local Similarity 27.1%; Pred. No. 0.0023;
Matches 19; Conservative 20; Mismatches 27; Indels 4; Gaps 3;

QY 1 KGVSLSYRCPCRFESHVARANKHLKILNTPN--C-AIQIVARLKNNNQVCIIDPKLW 57
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 27 RSLGVSLHRCICETESRPICRIKYSVEII-SPNSHCDKTEITITLADTGVELCLDPEAPW 85
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 58 IOEYLEKALN 67
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 86 VKRVINKLIS 95
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 6
Q90Y59 PRELIMINARY: PRT: 109 AA.
AC Q90Y59;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Interleukine-8.
GN IL-8.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralicthyidae; Paralicthys.
NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21435923; PubMed=11551708;
RA Lee E.Y., Park H.H., Kim Y.T., Chung J.K., Choi T.J.;
RT "Cloning and sequence analysis of the Interleukin-8 gene from flounder
  (Paralicthys olivaceus).";
RL Gene 274:237-243(2001).
DR EMBL: AF216646; AAL05442.1;
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.117 MW; C7CE18986C50A6ED CRC64;
SQ SEQUENCE 109 AA: 12117 MW: C7CE18986C50A6ED CRC64;

Query Match 24.5%; Score 88; DB 13; Length 109;
Best local Similarity 27.1%; Pred. No. 0.0026;
Matches 19; Conservative 20; Mismatches 27; Indels 4; Gaps 3;

QY 1 KGVSLSYRCPCRFESHVARANKHLKILNTPN--C-AIQIVARLKNNNQVCIIDPKLW 57
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 26 RSLGVSLHRCICETESRPICRIKYSVEII-SPNSHCDKTEITITLADTGVELCLDPEAPW 84
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 58 IOEYLEKALN 67
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 85 VKRVINKLIS 94
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 7
Q9YVA9 PRELIMINARY: PRT: 134 AA.
AC Q9YVA9;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE VIL8 (CXC chemokine VIL8).
GN MDV003 OR MDV078.
OS Gallid herpesvirus 1,
OS Marek's disease herpesvirus (strain GA) (MDHV), and
OS Marek's disease herpesvirus (strain Md5) (MDV). Turkey herpesvirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Infectious latyngotrichetis-like viruses.
NCBI_TaxID=10386, 10388, 10389;
RN [1]
RP SEQUENCE FROM N.A.
SQ SPECIES=callid herpesvirus 1; STRAIN=RB1B;

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RA Rasschaert D., Fagnant L.;
RT "Characterisation of the BamHI I fragment of the Marek's disease virus
  RB1B strain (serotype 1).";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Marek's disease herpesvirus (strain GA) (MDHV);
RA Lin S.-F., Robinson D., Chen H.-C., Kung H.-J.;
RT "CXC chemokine encoded by Marek's Disease Virus (MDV).";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Marek's disease herpesvirus (strain Md5) (MDV);
RX MEDLINE=20392152; PubMed=10933706;
RT Tulman E.R., Afonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
RL "The genome of a very virulent Marek's disease virus.";
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Marek's disease herpesvirus (strain Md5) (MDV);
RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF331499; AAL58097.1;
DR EMBL: AF065430; AAC77449.1;
DR EMBL: AF243438; AAG14290.1;
DR EMBL: AF243438; AAG14256.1;
DR HSSP: P10889; IM12.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXC_chemokine_sm11.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTKCXC.
DR SMART: SM00199; SCY; 1
SQ SEQUENCE 134 AA: 14828 MW: C859CDB86BD25190 CRC64;

Query Match 23.3%; Score 83.5; DB 12; Length 134;
Best local Similarity 25.9%; Pred. No. 0.011;
Matches 22; Conservative 14; Mismatches 12; Indels 37; Gaps 5;

QY 2 GVSLSYRCPCRFESHVARANKHLKILNTPN-----NC-AIQIV 39
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 22 GVSLSYRCPCRFESHVARANKHLKILNTPN-----VKVNRPTGLPIADVIPPICRTEII 67
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 40 ARLKNNNQVCIIDPKLWIOEYLEK 64
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 68 FALK-KNRKVCVDPPEAPWQDFIK 91
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
T9IBJ7 PRELIMINARY: PRT: 142 AA.
AC T9IBJ7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE VIL-8.
GN R-LOF2.
OS Turkey herpesvirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Marek's disease-like viruses.
NCBI_TaxID=10390;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GA;
RX MEDLINE=92237304; PubMed=1315048;
RA Jones D., Lee L., Liu J.L., Kung H.-J., Tillotson J.K.;
RT "Marek disease virus encodes a basic-leucine zipper gene resembling
  the fos/jun oncogenes that is highly expressed in lymphoblastoid
  tumors.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4042-4046(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GA;
RA Lee L.F., Wu P., Sui D., Ren D., Kung H.-J.;

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RT "The Complete UL Sequence of Serotype I Marek's Disease Virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2000).
DR EMBL: AF147806; AAF67205.1; -.
DR HSSP: P10889; IM12.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXCL1; Chemokine_sm11.
DR InterPro: IPR001230; Prey1_site.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTCKXC.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00294; PRENPLATION; UNKNOWN_1.
SQ SEQUENCE 142 AA; 15770 MW; 35A8CEB9B29FD209 CRC64;

Query Match
Best Local Similarity 23.3%; Score 83.5; DB 12; Length 142;
Matches 22; Conservative 14; Mismatches 12; Indels 37; Gaps 5;

QY 2 GVSL-----SYRCPCRFESHVARANVKHLKILNTP-----NC-ALQIV 39
DB 22 GISLESLAVDKRCCK-----VKVTNRPTGLGPIIADVPIPGIHRRTETI 67
QY 40 ARKNNRQVCIDPRKMKIOEYLER 64
DB 68 FALK-KNRKVCVDEAPWVOQFIKK 91

RESULT 9
073912 PRELIMINARY; PRT; 104 AA.
AC 073912;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE K60 protein precursor (CXCL chemokine K60).
GN K60.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RX NCB1
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MACROPHAGE LIKE;
RA Sick C.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20170941; Pubmed-10704244;
RA Sick C., Schneider K., Staeheli P., Weinig K.C.;
RT "Novel chicken CXCL and CC chemokines.";
RL Cytochrome 12:181-186(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Hughes S.M., Bumstead N.;
RT "Mapping of a second ELR CXCL chemokine to chicken chromosome four.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y14971; CAA75212.1; -.
DR EMBL: AF277660; AAF6485.1; -.
DR HSSP: P02775; ITVX.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXCL1; Chemokine_sm11.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTCKXC.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
KW Signal.
GN SIGNAL.
FT CHAIN 1 20 POTENTIAL.
FT CHAIN 21 104 K60 PROTEIN.
SQ SEQUENCE 104 AA; 11199 MW; 83725AB91FE18E3D CRC64;

Query Match
Best Local Similarity 23.1%; Score 83; DB 13; Length 104;
Matches 27.5%; Pred. No. 0.01;

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Matches 19; Conservative 20; Mismatches 22; Indels 8; Gaps 4;

QY 4 SLISYRCPCRFESHVARANVKHLKILNTP-----PNCALQIVARLKNRQVCIDPRKMKI 58
DB 29 AIELRCOC--LETHSKTRIFKFIQNVNLTPSGPCKNAVEIATLK-DGREYCLDPTAPMV 85
QY 59 QEYLEKALN 67
DB 86 KLIIKALD 94

RESULT 10
067634 PRELIMINARY; PRT; 203 AA.
AC 067634;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Eco Q protein (Fragment).
OS Marek's disease herpesvirus (strain GA) (MDHV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Marek's disease-like viruses.
OC NCBI_TaxID=10388;
RX NCB1
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GA;
RX MEDLINE=96074534; Pubmed-7491783;
RA Peng Q., Zeng M., Bhuiyan Z.A., Ubukata E., Tanaka A., Nonoyama M.,
RA Shirazi Y.;
RT "Isolation and characterization of Marek's disease virus (MDV) cDNAs
RT mapping to the BamHI-12, BamHI-Q2, and BamHI-L fragments of the MDV
RT genome from lymphoblastoid cells transformed and persistently infected
RT with MDV.";
RL Virology 213:590-599(1995).
DR EMBL: U34966; AAC54629.1; -.
DR HSSP: P10889; IM12.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXCL1; Chemokine_sm11.
DR InterPro: IPR004827; TFC_bZIP.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTCKXC.
DR SMART: SM00338; BRLZ; 1.
DR SMART: SM00199; SCY; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 203 AA; 23132 MW; DE42FE2A1C1A71C88 CRC64;

Query Match
Best Local Similarity 23.1%; Score 83; DB 12; Length 203;
Matches 19; Conservative 17; Mismatches 13; Indels 32; Gaps 4;

QY 1 KGVSLSYRCPCRFESHVARANVKHLKILNTP-----NC-ALQIVARLK 43
DB 95 ESLAVDKRCCK-----VKVTNRPTGLGPIIADVPIPGIHRRTETIIPALK 140
QY 44 NNNRQVCIDPRKMKIOEYLER 64
DB 141 -KNRKVCVDEAPWVOQFIKK 160

RESULT 11
090YD7 PRELIMINARY; PRT; 148 AA.
AC 090YD7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Small inducible cytokine A2.
GN SCY42.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.  
 RC STRAIN-SJL/J; TISSUE=SPLEEN;  
 RX MEDLINE=99370037; PubMed=10438970;  
 RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,  
 RA Blankenhorn E.P.;  
 RT "Sequence polymorphisms in the chemokines Sclay (TCA-3), Sclay2  
 RT (monocyte chemoattractant protein (MCP)-1), and Sclay12 (MCP-5) are  
 RT candidates for eae7, a locus controlling susceptibility to monophasic  
 RT remitting/nonrelapsing experimental allergic encephalomyelitis.";  
 RL J. Immunol. 163:2262-2266(1999).  
 DR EMBL: AF065929; AAF15379.1; -;  
 DR HSSP: P13500; 1DOK.  
 DR MGD: MGI:98259; Scya2.  
 DR InterPro: IPR000827; CC\_chemokine\_sml.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PF00048; IL8; 1.  
 DR SMART: SM00199; SCY; 1.  
 DR PROSITE: PS00472; SMALL\_CYTOKINES\_CC; 1.  
 SQ SEQUENCE 148 AA; 16268 MW; 2BA24C5D19C489EB CRC64;

Query Match 22.3%; Score 80; DB 11; Length 148;  
 Best Local Similarity 24.6%; Pred. No. 0.034;  
 Matches 15; Conservative 14; Mismatches 32; Indels 0; Gaps 0;

OY 3 VSLSYRCPRFESHVARANVKHLILNTPNCALQIVARLKNNNROVCIIDPKLWIOEYL 62  
 DB 28 VNAPLTCCISFTSKMIPMSRLEGYKRITSSRCPEKAVVFYTKLREVCADPKKEWQYTI 87  
 OY 63 E 63  
 DB 88 K 88

RESULT 12  
 OY3442 PRELIMINARY; PRT; 101 AA.  
 AC OY3442;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE LFCA-1 protein precursor.  
 OS Lamprol fluvialilis (River lamprey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
 OC Petromyzontiformes; Petromyzontidae; Lampetra.  
 OX NCBI\_TaxId=7748;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LEUCOCYTES;  
 RA Na)kshin A.M., Mechetina L.V., Alabyev B.Y., Taranin A.V.;  
 RT "Identification of the interleukin 8 homologue of chemokines";  
 RT fluvialilis): early evolutionary divergence of chemokines";  
 RL Submitted (JUL-1998) to the EMBL/Genbank/DBD databases.  
 DR EMBL: AJ231072; CAA13114.1; -;  
 DR HSSP: P02775; 1TVX.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR InterPro: IPR001089; CXC\_chemkine\_sml.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTKXC.  
 DR SMART: SM00199; SCY; 1.  
 DR SIGNAL.  
 KW SIGNAL.  
 FT CHAIN 1 22 POTENTIAL.  
 SQ SEQUENCE 101 AA; 11095 MW; 80CFEEB1EA7336D2 CRC64;

Query Match 22.1%; Score 79.5; DB 13; Length 101;  
 Best Local Similarity 26.9%; Pred. No. 0.027;  
 Matches 18; Conservative 16; Mismatches 22; Indels 11; Gaps 4;

OY 8 RCRCRFESHVARANV--KHLK----ILNTPNCA-LQIVARLKNNNROVCIIDPKLWIOE 60  
 DB 30 RCRC----VAVISKFTHPKHFMTEVYIPSSNCKNVEIITVMKSTNNQICLNDADAVRK 85  
 OY 61 YLEKALN 67

DB 86 VISHLD 92

RESULT 13  
 OY28724 PRELIMINARY; PRT; 108 AA.  
 AC OY28724;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1999 (TREMBLrel. 11, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE GRO (Permeability factor 2).  
 GN RPF2.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxId=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NEW ZEALAND WHITE;  
 RA Yoshimura T., Modi W.S.;  
 RT "Isolation of novel GRO genes, and a phylogenetic analysis of the CXC  
 RT chemokine subfamily in mammals.";  
 RL Submitted (MAR-1997) to the EMBL/Genbank/DBD databases.  
 RN [2]  
 RP SEQUENCE OF 43-108 FROM N.A.  
 RC STRAIN=NEW ZEALAND WHITE;  
 RX MEDLINE=95129889; PubMed=7828903;  
 RA Johnson M.C., Goodman R.B. II, Kajikawa O., Wong V.A., Mongovin S.M.,  
 RA Martin T.R.;  
 RT "Cloning of two rabbit GRO homologues and their expression in alveolar  
 RT macrophages";  
 RL Gene 151:337-338(1994).  
 DR EMBL: U95808; AAB93924.1; -;  
 DR EMBL: L28933; AAB66975.1; -;  
 DR HSSP: P19875; 1ONK.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR InterPro: IPR001089; CXC\_chemkine\_sml.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTKXC.  
 DR SMART: SM00199; SCY; 1.  
 DR PROSITE: PS00471; SMALL\_CYTOKINES\_CC; 1.  
 SQ SEQUENCE 108 AA; 11261 MW; 9C278041FC7A5BAD CRC64;

Query Match 22.1%; Score 79.5; DB 6; Length 108;  
 Best Local Similarity 27.4%; Pred. No. 0.023;  
 Matches 17; Conservative 21; Mismatches 21; Indels 3; Gaps 3;

OY 8 RCRCRFESHVARANVKHLILNTPNCA-LQIVARLKNNNROVCIIDPKLWIOEYLEKA 65  
 DB 43 RCOCLOTVOGIIHLKSIQSLKVLSPGHCAOTEVIALTK-SGDEACLNPAAPVKKFLQKR 101  
 OY 66 LN 67  
 DB 102 LS 103

RESULT 14  
 OY98702 PRELIMINARY; PRT; 97 AA.  
 AC OY98702;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Putative Interleukin 8 (Putative cxc chemokine precursor).  
 GN IL-8.  
 OS Onchorynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Actinopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxId=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A.

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RA Laing K.J., Zou J.J., Hirono I., Aoki T., Secombes C.J.;
RT "Identification and analysis of the interleukin 8 molecule in rainbow
RL trout Oncorhynchus mykiss.";
RN Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Sangrador-Vegas A., Smith T.J.;
RT "Molecular cloning of a rainbow trout (Oncorhynchus mykiss) CX
RL chemokine by use of suppression subtractive hybridization.";
RN Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RA Laing K.J., Zou J.J., Hirono I., Aoki T., Secombes C.J.;
RT "Identification and analysis of the interleukin 8 molecule in rainbow
RL trout Oncorhynchus mykiss.";
RN Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ279069; CAC33585.1; -
DR EMBL; AJ300835; CAC45061.1; -
DR EMBL; AJ310565; CAC83945.1; -
DR HSSP; P19875; IONK.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR001089; CXK_chmkine_sml.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTCKXC.
DR SMART; SM00199; SCY; 1.
DR SIGNAL.
FT CHAIN 1 22 POTENTIAL.
FT SIGNAL 23 97 PUTATIVE CXK CHEMOKINE.
SQ SEQUENCE 97 AA: 10777 MW: 4EBB35A4EF9DACE2 CRC64;

Query Match 22.0%; Score 79; DB 13; Length 97;
Best Local Similarity 25.0%; Pred. No. 0.03;
Matches 17; Conservative 18; Mismatches 31; Indels 2; Gaps 2;

OY 1 KGVSLSTPCPCRFESHVARNVKKHLKLTNPNCALQIVARLKNNROYCIDPKLKI 58
Db 26 RGMGADLCRCIEETESRRIGRLKRVEMFPSPSCHRDEITATLSKSGEICLDVSAPW 85
OY 59 OEYLEKAL 66
Db 86 KRVIKML 93

RESULT 15
O92318
ID O92318 PRELIMINARY; PRT; 97 AA.
AC O92318;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Monocyte chemoattractant protein-3 (MCP-3).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Asano K., Nakamura M., Oguma T., Fukunaga K., Matsubara H.,
RA Ishizaka A., Yamaguchi K., Kanazawa M.;
RT "Differential expression of CC chemokines in guinea pig lungs during
RT an allergic inflammation.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB014340; BAA36456.1; -
DR HSSP; P51671; ILOT.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 97 AA: 11159 MW: E1B9A17C165C2421 CRC64;

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Query Match 21.9%; Score 78.5; DB 11; Length 97;
Best Local Similarity 30.3%; Pred. No. 0.034;
Matches 20; Conservative 13; Mismatches 28; Indels 5; Gaps 2;

OY 2 KGVSLSTPCPCRFESHVARNVKKHLKLTNPNCALQIVARLKNNROYCIDPKLKI 60
Db 27 GVNISTCCYKRSQRIRVQR--LESYTRITSSKCPMAVIFKTKFNREICADPPKQWQDS 84
OY 61 --YLEK 64
Db 85 MKYIDK 90

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Search completed: January 23, 2003, 15:36:19  
 Job time : 24.6 secs

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OM protein - protein search, using sw model

Run on: January 23, 2003, 15:27:48 : Search time 28.2 seconds  
(without alignments)  
316.588 Million cell updates/sec

Title: US-09-852-424-2

Perfect score: 362  
Sequence: 1 KGVSPSYRCPCRFESHVAR.....QVCIDPKLKIQETYLEKALN 67

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A-Geneseq-101002:\*

1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:\*  
2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:\*  
3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:\*  
4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:\*  
5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:\*  
6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:\*  
7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:\*  
8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:\*  
9: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:\*  
10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:\*  
11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:\*  
12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:\*  
13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:\*  
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15: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:\*  
16: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:\*  
17: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:\*  
18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:\*  
19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:\*  
20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:\*  
21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\*  
22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*  
23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	362	100.0	67	23	AAW48657
2	352	97.2	67	23	AAW48656
3	347	95.9	67	23	AAW48658
4	345	95.3	67	23	AAW48660
5	344	95.0	67	19	AAW50760
6	344	95.0	67	20	AAW34092
7	344	95.0	67	20	AAV06741
8	344	95.0	67	20	AAV06726
9	344	95.0	67	21	AAV67594
10	344	95.0	67	23	AAW47680

11	344	95.0	68	19	AAW50761	Peptide which bind
12	344	95.0	69	20	AAV05818	N-terminal modifie
13	344	95.0	72	19	AAW50762	Peptide which bind
14	344	95.0	72	20	AAW34093	Native stromal cel
15	344	95.0	72	21	AAV67595	SDF-beta peptide
16	344	95.0	73	19	AAW50763	Peptide which bind
17	344	95.0	73	20	AAV05819	N-terminal modifie
18	344	95.0	74	21	AAV69041	Amino acid sequenc
19	344	95.0	89	16	AAW75419	Human SDF-1-alpha.
20	344	95.0	89	20	AAV39995	Human SDF-1-alpha
21	344	95.0	89	20	AAV26177	Stromal cell deriv
22	344	95.0	89	21	AAW15791	Human chemokine SD
23	344	95.0	89	21	AAV93603	A human B-cell sti
24	344	95.0	89	21	AAV52508	Human stromal cell
25	344	95.0	90	20	AAV05820	N-terminal modifie
26	344	95.0	93	16	AAW75420	Human SDF-1-beta.
27	344	95.0	93	19	AAW50766	Human SDF-1 which
28	344	95.0	93	20	AAV26178	Stromal cell deriv
29	344	95.0	93	20	AAV06725	Amino acid sequenc
30	344	95.0	93	21	AAW15812	Human chemokine SD
31	344	95.0	93	23	AAW23952	Human stromal cell
32	344	95.0	93	23	AAW84305	Human endometrial
33	344	95.0	93	23	AAW47690	SDF-1 precursor.
34	344	95.0	93	23	AAW47691	SDF-1-beta. Homo
35	344	95.0	94	20	AAV05821	N-terminal modifie
36	344	95.0	101	23	AAW48051	SDF-1gamma SEQ ID
37	344	95.0	119	23	AAW48047	Human SDF-1gamma S
38	344	95.0	166	20	AAV29899	Human SDF-1 beta a
39	344	95.0	177	20	AAV29896	Human SDF1 and hum
40	344	95.0	320	21	AAV69055	A chemokine recept
41	344	95.0	322	21	AAV69056	A chemokine recept
42	344	95.0	326	19	AAW76221	Human chemokine SD
43	344	95.0	327	21	AAV69057	A chemokine recept
44	344	95.0	328	19	AAW76220	Human chemokine SD
45	344	95.0	339	20	AAV29905	Human SDF-1 and hu

#### ALIGNMENTS

RESULT 1	
AAW48657	
ID	AAW48657 standard; peptide: 67 AA..
AC	AAW48657;
XX	
20-MAY-2002 (first entry)	
XX	
DE	CXCR4 peptide antagonist SEQ ID NO 2.
XX	
KW	CRX4; haematopoietic cell; chemokine receptor-4; cytostatic;
KW	Immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
XX	cell multiplication.
OS	Synthetic.
XX	
FT	Key
FT	Modified-site
FT	Location/Qualifiers
FT	5
FT	/note="Optionally the proline analogue 6-amino-7-oxo-2,3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic acid residue or a bicyclic turned dipeptide (Btd)"
XX	
XX	WO200185196-A2.
PN	
15-NOV-2001.	
PD	
XX	
09-MAY-2001; 2001WO-CA00659.	
XX	
09-MAY-2000; 2000CA-2305787.	
PR	
19-MAY-2000; 2000US-205467P.	
XX	
PA	(UYBR-) UNIV BRITISH COLUMBIA.

PA	(CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX	
PI	Tudán CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
PI	Clark-Lewis I, Salari H;
XX	
DR	WPI; 2002-106073/14.
XX	
PT	Promoting the rate of haematopoietic cell multiplication for treating a
PT	cancer involves administering chemokine receptor antagonist to the
PS	cells -
PS	Claim 9; page 54; 68pp; English.
XX	
CC	The invention relates to a method of promoting the rate of haematopoietic
CC	cell multiplication comprising administering chemokine receptor-4 (CXCR4)
CC	antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist
CC	has cytostatic and immunosuppressive activity and is useful for treating
CC	cancer or autoimmune disease in a patient; to promote the rate of
CC	haematopoietic cell multiplication; to formulate a medicament for
CC	increasing the circulation of the haematopoietic cells in a patient; for
CC	mobilising haematopoietic cells from a narrow locus to a peripheral blood
CC	locus; in the treatment of haematopoietic cells in vitro and in vivo. The
CC	CXCR4 antagonists stimulates haematopoietic cell multiplication,
CC	self-renewal, expansion and proliferation of peripheralisation in vivo.
XX	
SQ	Sequence 67 AA:
	Query Match 100.0%; Score 362; DB 23; Length 67;
	Best Local Similarity 100.0%; Pred.No. 1.9e-40;
	Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 KGVSPSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNRRQVCIDPKLKWIG 60 
DB	1 KGVSPSYRCPCRFESHVARANKHLKIINTPMCALQIVARLKNRRQVCIDPKLKWIG 60 
OY	61 YLEKALN 67 
DB	61 YLEKALN 67
	RESULT 2
AAM48656	
ID	AAM48656 standard; peptide; 67 AA.
XX	
AC	AAM48656;
XX	
DT	20-MAY-2002 (first entry)
XX	
DE	CXCR4 peptide antagonist SEQ ID NO 1.
XX	
KW	CRCX4: haematopoietic cell; chemokine receptor-4; cytostatic;
KW	immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
RN	cell multiplication.
XX	
OS	Synthetic.
XX	
PN	WO200185196-AZ.
PD	15-NOV-2001.
XX	
PE	09-MAY-2001; 2001WO-CA00659.
XX	
PR	09-MAY-2000; 2000CA-2305787.
XX	
PR	19-MAY-2000; 2000US-205467P.
XX	
PA	(UYBR-) UNIV BRITISH COLUMBIA.
PA	(CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX	
PI	Tudán CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
XX	
PI	Clark-Lewis I, Salari H;
XX	
DR	WPI; 2002-106073/14.

Pt	Promoting the rate of haematopoietic cell multiplication for treating a
Pt	cancer involves administering chemokine receptor antagonist to the
Pt	cells -
Pt	Claim 9; page 54; 68pp; English.
xx	
xx	The invention relates to a method of promoting the rate of haematopoietic
CC	cell multiplication comprising administering chemokine receptor-4 (CXCR4)
CC	antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist
CC	has cytosolic and immunosuppressive activity and is useful for treating
CC	cancer or autoimmune disease in a patient; to promote the rate of
CC	haematopoietic cell multiplication; to formulate a medicament for
CC	increasing the circulation of the haematopoietic cells in a patient; for
CC	localising haematopoietic cells from a narrow locus to a peripheral blood
CC	locus; in the treatment of haematopoietic cells in vitro and in vivo. The
CC	CXCR4 antagonists stimulates haematopoietic cell multiplication,
CC	self-renewal, expansion and proliferation of peripheralisation in vivo.
CC	
SQ	Sequence 67 AA:
Query Match	97.2%; Score 352; DB 23; Length 67;
Best Local Similarity	98.5%; Pred. No. 4e-39;
Matches 66; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1 KGVSYRCPCPFESHVARANVKHLKILTPNCALQIYARLKNRRVCIDPKLKWIOE 60       1 KGVSYRCPCHREFSHVARANVKHLKILTPNCALQIYARLKNRRVCIDPKLKWIOE 60
Db	61 YLEKALN 67         61 YLEKALN 67
DR	
RESULT 3	
AAM48658	ID AAM48658 standard; peptide; 67 AA.
XX	AAM48658;
AC	
XX	20-MAY-2002 (first entry)
DT	
XX	CXCR4 peptide antagonist SEQ ID NO 3.
DE	
XX	CXCR4; haematopoietic cell; chemokine receptor-4; cytostatic;
KW	immunosuppressive; cancer; autoimmune disease; peripheral blood locus;
KW	cell multiplication.
XX	
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 6 /note= "Optionally the proline analogue 6-amino-7-oxo-2,
FT	3,4,5,6,7-hexahydro-1H-indoline-1-carboxylic
FT	acid residue or a bicyclic turned dipeptide
FT	(Bld)"
PN	WO200185196-AZ.
PD	
PD	15-NOV-2001.
PF	
PF	09-MAY-2001; 2001WO-CA00659.
PR	
PR	09-MAY-2000; 2000CA-2305787.
PR	19-MAY-2000; 2000US-205467P.
PA	
PA	(UYBR-) UNIV BRITISH COLUMBIA.
PA	(CHEM-) CHEMOKINE THERAPEUTICS CORP.
PI	Tudon CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;
PI	Clark-Lewis I, Salari H;
XX	
DR	WPI; 2002-106073/14.
XX	



CC associated opportunistic infections and/or other CXC or CC chemokines,  
 CC especially RANTES, MIP1- alpha, MIP1- beta or MCP1. The peptide can be  
 CC used to detect anti-SDF-1 antibodies in biological fluids. This  
 CC sequence represents a specifically claimed peptide which binds to the  
 CC CXCR4 receptor.

XX  
 SQ Sequence 67 AA;

Query Match 95.0%; Score 344; DB 19; Length 67;  
 Best Local Similarity 97.0%; Pred. No. 4.7e-38;  
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPSYRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 DB 1 KPVLSYRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67  
 DB 61 YLEKALN 67

RESULT 6  
 AAY34092  
 ID AAY34092 standard; protein; 67 AA.

AC AAY34092;  
 XX  
 DT 29-NOV-1999 (first entry)

DE Native stromal cell derived factor 1 (SDF-1) alpha protein.

XX CXC chemokine receptor 4; CXCR4; antagonist; medicament; T-cell;  
 KM interferon gamma; autoimmune disease; multiple sclerosis; cancer;  
 KM angiogenesis; stromal cell derived factor 1; SDF-1.

XX Mammalia.

XX WO947158-A2.

XX 23-SEP-1999.

PF 12-MAR-1999; 99WO-CA00221.

XX 13-MAR-1998; 98CA-2226391.

PR 14-AUG-1998; 98CA-2245224.

XX (UYBR-) UNIV BRITISH COLUMBIA.

PI Clark-Lewis I, Gong J, Durotojo V;

DR WPI; 1999-561857/47.

PT Use of CXC chemokine receptor 4 for treating autoimmune disease and

PT cancer -

XX Example 1; Fig 1; 71pp; English.

CC The invention relates to the use of a CXC chemokine receptor 4 (CXCR4)  
 CC antagonist for the manufacture of a medicament for reducing interferon  
 CC gamma production by T-cells in a mammal. The CXCR4 antagonist can be used  
 CC to treat or to design a medicament to treat, an autoimmune disease,  
 CC multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4  
 CC antagonists may be peptide compounds comprising a substantially purified  
 CC peptide fragment, analogue or a pharmacologically acceptable salt of  
 CC stromal cell derived factor 1 (SDF-1). The present sequence represents  
 CC the amino acid sequence of SDF-1 alpha protein.

XX  
 SQ Sequence 67 AA;

Query Match 95.0%; Score 344; DB 20; Length 67;  
 Best Local Similarity 97.0%; Pred. No. 4.7e-38;  
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPSYRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 DB 1 KPVLSYRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67  
 DB 61 YLEKALN 67

RESULT 7  
 AAY06741  
 ID AAY06741 standard; protein; 67 AA.

AC AAY06741;  
 XX  
 DT 18-JUN-1999 (first entry)

DE SDF-1 alpha/RANTES cross-over chemokine control molecule SSSS.

XX Chemokine; cross-over protein; pharmaceutical; inflammatory; AIDS; viral;  
 KM infectious disease; hematopoiesis; chemoprotection; asthma; RANTES; VMP;  
 KM allergic rhinitis; atopic dermatitis; rheumatoid arthritis; SDF-1; MPV;  
 KM stromal cell derived factor 1; Macrophage Inflammatory protein.

XX Synthetic.  
 OS Homo sapiens.

XX WO9911655-A1.

PD 11-MAR-1999.

PF 31-AUG-1998; 98WO-US18096.

XX 04-SEP-1997; 97US-0057620.

PR (GRYP-) GRYPHON SCI.

XX Kent SBH, Stani MA, Simon R, Wilken J;

DR WPI; 1999-205128/17.

XX New cross-over proteins for treatment of inflammation and infections

PT e.g. AIDS - prepared by ligation of two functional protein modules

PT derived from two different parent molecules

XX Example 4; Page 43; 75pp; English.

CC The invention relates to a cross-over protein produced by chemical  
 CC ligation of at least two functional protein modules derived from at  
 CC least two parent protein molecules. The cross-over proteins can be used  
 CC in pharmaceutical compositions for therapy of inflammatory and  
 CC infectious diseases including AIDS, and for indications of hematopoiesis  
 CC and chemoprotection. They are also useful for treatment of asthma,  
 CC allergic rhinitis, atopic dermatitis and rheumatoid arthritis. A library  
 CC comprising a collection of cross-over proteins is useful for screening  
 CC for cross-over proteins that are receptor ligands. The libraries  
 CC comprise functionally diverse compounds therefore improving the drug  
 CC discovery process. The proteins and libraries are exemplified by the  
 CC preparation of cross-over chemokines comprising various combinations of  
 CC peptide segments derived from RANTES, SDF-1 (stromal cell derived factor  
 CC 1), VMP (viral Macrophage Inflammatory protein) and other such  
 CC chemokines. Sequences AAY06741-62 represent amino acid sequences of SDF-1  
 CC alpha/RANTES cross-over molecules.

XX  
 SQ Sequence 67 AA;

Query Match 95.0%; Score 344; DB 20; Length 67;  
 Best Local Similarity 97.0%; Pred. No. 4.7e-38;  
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPSYRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 DB 1 KPVLSYRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67  
 DB 61 YLEKALN 67

# RESULT 8

AAV06726  
 ID AAV06726 standard; protein; 67 AA.

AAV06726;

18-JUN-1999 (first entry)

XX Amino acid fragment of SDF-1 alpha.

XX Chemokine; cross-over protein; pharmaceutical; inflammatory; AIDS; viral;  
 KW Infectious disease; hematopoiesis; chemoprotection; asthma; RANTES; VMIPI;  
 KW allergic rhinitis; atopic dermatitis; rheumatoid arthritis; SDF-1; MPV;  
 KW stromal cell derived factor 1; Macrophage Inflammatory protein.

OS Homo sapiens.  
 OS Synthetic.

PN WO9911655-A1.

XX 11-MAR-1999.

PF 31-AUG-1998; 98WO-US18096.

PR 04-SEP-1997; 97US-0057620.

XX (GRYP-) GRYPHON SCI.

PI Kent SBH, Stanl MA, Simon R, Wilken J;

DR WPI: 1999-205128/17.

PT New cross-over proteins for treatment of inflammation and infections  
 PT e.g. AIDS - prepared by ligation of two functional protein modules  
 PT derived from two different parent molecules

XX Example 4; Page 41; 75pp; English.

CC The invention relates to a cross-over protein produced by chemical  
 CC ligation of at least two functional protein modules derived from at least  
 CC two parent protein molecules. The cross-over proteins can be used in  
 CC pharmaceutical compositions for therapy of inflammatory and infectious  
 CC diseases including AIDS, and for indications of hematopoiesis and  
 CC chemoprotection. They are also useful for treatment of asthma, allergic  
 CC rhinitis, atopic dermatitis and rheumatoid arthritis. A library  
 CC comprising a collection of cross-over proteins is useful for screening  
 CC for cross-over proteins that are receptor ligands. The libraries comprise  
 CC functionally diverse compounds therefore improving the drug discovery  
 CC process. The proteins and libraries are exemplified by the preparation  
 CC of cross-over chemokines comprising various combinations of peptide  
 CC segments derived from RANTES, SDF-1 (stromal cell derived factor 1), VMIPI  
 CC (viral Macrophage Inflammatory protein) and other such chemokines. The  
 CC present sequence represents an amino acid fragment of SDF-1 alpha which  
 CC acts as a synthetic base molecule for synthesising the cross-over  
 CC protein.

XX Sequence 67 AA:

## Query Match

Best Local Similarity 95.0%; Score 344; DB 20; Length 67;  
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPSYRCPCRFESHVARANKHLKILNTPCALQIVARLKNNNROVCIDPKLWIOE 60  
 DB 1 KPVSLSYRCPCRFESHVARANKHLKILNTPCALQIVARLKNNNROVCIDPKLWIOE 60  
 OY 61 YLEKALN 67

DB 61 YLEKALN 67

# RESULT 9

AAV67594  
 ID AAV67594 standard; peptide; 67 AA.

AAV67594;

13-JUN-2000 (first entry)

XX SDF-1alpha peptide sequence.

XX SDF-1; CXCR4; CXCR4 chemokine receptor 4; gamma-interferon; cancer; gout;  
 KW autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;  
 KW type 1 diabetes; ulcerative colitis; lupus; angiotensin; antitumour;  
 KW stromal cell derived factor one; anti-inflammatory; immunomodulatory.

OS Unidentified.

PN WO200009152-A1.

XX 24-FEB-2000.

PF 16-AUG-1999; 99WO-CA00750.

PR 14-AUG-1998; 98CA-2245224.

PA (UYBR-) UNIV BRITISH COLUMBIA.

PI Clark-Lewis I, Gong J, Duronio V, Salari H;

DR WPI: 2000-224175/19.

PT Therapeutic composition containing CXCR4 antagonist, useful for  
 PT treating autoimmune disease, especially multiple sclerosis and cancer

XX Disclosure; Fig 1; 88pp; English.

CC The invention provides a therapeutic composition containing an antagonist  
 CC of CXCR4 (CXCR4 chemokine receptor 4) and an excipient. The compositions  
 CC are specifically used to reduce production of gamma-interferon by T  
 CC cells, particularly for treating autoimmune disease, especially multiple  
 CC sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral  
 CC sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative  
 CC colitis, gout, lupus and transplant rejection; to treat cancer by  
 CC inhibiting angiogenesis; inhibition of restenosis; and when labeled, to  
 CC evaluate in vivo pharmacokinetics, or to determine disease progression  
 CC and susceptibility, or as targeting agents for delivery of other  
 CC therapeutic agents. The antagonist is selected from SDF-1 (stromal cell  
 CC derived factor one) peptide fragments, SDF-1 being the only known natural  
 CC ligand for CXCR4. The present sequence represents a SDF-1alpha  
 CC peptide sequence.

XX Sequence 67 AA:

## Query Match

Best Local Similarity 95.0%; Score 344; DB 21; Length 67;  
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPSYRCPCRFESHVARANKHLKILNTPCALQIVARLKNNNROVCIDPKLWIOE 60

DB 1 KPVSLSYRCPCRFESHVARANKHLKILNTPCALQIVARLKNNNROVCIDPKLWIOE 60

OY 61 YLEKALN 67

DB 61 YLEKALN 67

RESULT 10  
 AAB47680

ID AAB47680 standard; peptide: 67 AA.  
XX AAB47680;  
AC  
XX  
XX 30-JAN-2002 (first entry)  
DT  
XX SDF-1-alpha.  
DE  
XX  
XX Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;  
KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;  
KM macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;  
KW autologous; allogenic; bone marrow; stem cell; transplantation.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200176615-A2.  
PN  
XX 18-OCT-2001.  
PD  
XX  
XX 12-APR-2001; 2001WO-CA00540.  
PF  
XX  
XX 12-APR-2000; 2000CA-2305036.  
PR 14-SEP-2000; 2000US-232425P.  
PR 23-FEB-2001; 2001CA-2335109.  
XX  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
XX  
XX Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ,  
PI Cashman J, Clark-Lewis I;  
XX  
XX WPI; 2002-025882/03.  
DR  
XX  
XX CXC receptor 4 agonists that reduces hematopoietic cell multiplication  
PT and susceptibility to cytotoxic agents, are useful for bone marrow or  
PT peripheral blood stem cell transplantation -  
XX  
XX  
XX Claim 8; Page 57; 74pp; English.  
PS  
XX  
XX The sequences given in AAB47680-717 represent peptides which may be  
CC used in the method of the invention for reducing the rate of  
CC hematopoietic cell multiplication. These peptides act as CXC chemokine  
CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on  
CC stromal cell derived factor one (SDF-1) with some also containing  
CC sequences derived from macrophage inflammatory protein 1-alpha  
CC (MIP-1-alpha). They can be used to reduce susceptibility of  
CC hematopoietic cells to a cytotoxic agent, by administering one of the  
CC agonist peptides to the cells prior to or during exposure of the  
CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce  
CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly  
CC in a patient with cancer requiring autologous or allogenic bone marrow  
CC or peripheral blood stem cell transplantation, or an autoimmune disease.  
XX  
XX  
XX Sequence 67 AA;  
SQ  
Query Match 95.0%; Score 344; DB 23; Length 67;  
Best Local Similarity 97.0%; Pred. No. 4.7e-38;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSPSYRCPCRFESHVARANKHKLTPNCALQIVARLKNNNQVCIDPKLKWIOE 60  
DB 1 KPVSLSYRCPCRFESHVARANKHKLTPNCALQIVARLKNNNQVCIDPKLKWIOE 60  
DB 1 KPVSLSYRCPCRFESHVARANKHKLTPNCALQIVARLKNNNQVCIDPKLKWIOE 60  
QY 61 YLEKALN 67  
DB 61 YLEKALN 67

RESULT 11  
AAW50761  
ID AAW50761 standard; peptide: 68 AA.  
XX  
XX AAW50761;  
AC

XX 27-JUL-1998 (first entry)  
DT  
XX  
XX Peptide which binds to CXCR4 receptor and is useful for treating HIV.  
DE  
XX  
XX Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus;  
KW HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.  
XX  
XX Homo sapiens.  
OS  
XX  
XX FR2751658-A1.  
PN  
XX 30-JAN-1998.  
PD  
XX  
XX 26-JUL-1996; 96FR-0009477.  
PF  
XX  
XX 26-JUL-1996; 96FR-0009477.  
PR  
XX (INSP ) INST PASTEUR.  
XX  
XX Arenzana SF, Baggiolini M, Clark LI, Moser B, Virelizier JL;  
PI  
XX  
XX WPI; 1998-123039/12.  
DR  
XX  
XX Human stromal cell-derived chemokine, SDF-1 - useful for treating  
PT human immunodeficiency virus infection  
PT  
XX  
XX Claim 5; Page 29; 48pp; French.  
PS  
XX  
XX The invention relates to peptides which bind to a cellular receptor for  
CC CXC chemokines, namely the CXCR4 receptor (also known as leukocyte-  
CC expressed transmembrane domain receptor), especially where the  
CC peptide is human chemokine SDF-1. The peptide can be used to treat or  
CC prevent HIV infections, optionally together with reverse transcriptase  
CC inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4  
CC receptor antagonists, immunotherapy agents, agents for treating HIV-  
CC associated opportunistic infections and/or other CXC or CC chemokines,  
CC especially RANTES, MIP-1 alpha, MIP-1 beta or MCP1. The peptide can be  
CC used to detect anti-SDF-1 antibodies in biological fluids. This  
CC sequence represents a specifically claimed peptide which binds to the  
CC CXCR4 receptor.  
XX  
XX  
XX Sequence 68 AA;  
SQ  
Query Match 95.0%; Score 344; DB 19; Length 68;  
Best Local Similarity 97.0%; Pred. No. 4.7e-38;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSPSYRCPCRFESHVARANKHKLTPNCALQIVARLKNNNQVCIDPKLKWIOE 60  
DB 2 KPVSLSYRCPCRFESHVARANKHKLTPNCALQIVARLKNNNQVCIDPKLKWIOE 61  
DB 2 KPVSLSYRCPCRFESHVARANKHKLTPNCALQIVARLKNNNQVCIDPKLKWIOE 61  
QY 61 YLEKALN 67  
DB 62 YLEKALN 68

RESULT 12  
AAW05818  
ID AAW05818 standard; protein: 69 AA.  
XX  
XX AAW05818;  
AC  
XX  
XX 02-AUG-1999 (first entry)  
DT  
XX  
XX N-terminal modified chemokine met-hSDF-1 alpha.  
DE  
XX  
XX Stromal cell-derived factor 1 alpha; SDF-1 alpha; met-hSDF-1 alpha;  
KW human; protein engineering; amino-terminal modification; mutant;  
KW HIV; infection; angiogenesis; autoimmune disease; inflammation;  
KW antiangiogenic; antiinflammatory; immunosuppressive; therapy;  
XX  
XX vaccine.  
XX



OS	Homo sapiens.
CS	Synthetic.
XX	
PN	M09920759-AI.
PD	29-APR-1999.
XX	
PF	21-OCT-1998; 98MO-US22282.
XX	
PR	20-OCT-1998; 98US-0175713.
PR	22-OCT-1997; 97US-0955826.
PR	27-FEB-1998; 98WO-USO4002.
PA	(GEMV ) GENETICS INST INC.
XX	
P1	Herrmann SH, Lu Z, McCoy JM, Swanberg SL, Walker B;
P1	Yang Oj;
DR	WPI: 1999-298307/24.
DR	N-PDB: AAX2530.
XX	
PT	Modified chemokines useful for inhibiting or stimulating
PT	angiogenesis
XX	
PS	ClaIm 6c; Page 79; 85pp; English.
XX	
CC	The present sequence represents met-hSDF-1 alpha, i.e., human
CC	stromal cell derived growth factor-1 alpha having an added
CC	N-terminal methionine residue. DNA encoding met-hSDF-1 alpha (see
CC	AAX2530) was produced by cloning an NdeI/XbaI-restricted hSDF-1
CC	alpha PCR product into the E. coli expression vector pAL781
CC	In-frame with an ATC codon. met-hSDF-1 alpha is an example of
CC	novel N-terminal modified chemokines (see AAY05818-21) that have at
CC	least one Met residue, at least one aminoxy-pentane residue or at
CC	least one GroHK peptide (see AAY05822) covalently attached at the
CC	N-terminus. The N-terminal modified chemokines are useful for
CC	altering receptor function, inhibiting interactions between
CC	chemokine receptors and their ligands. They are used as research
CC	tools for identifying chemokine receptors, as vaccine adjuvants, as
CC	agents for the chemotactic recruitment of migratory cells, as agents
CC	for the stimulation or inhibition of angiogenesis, as agents against
CC	autoimmune diseases and inflammation, and as agents to inhibit the
CC	binding of HIV to certain receptors and the infection of
CC	susceptible cells by HIV. HIV infection is best treated with
CC	modified SDF-1 alpha and beta or MIP-1 alpha and beta.
CC	
XQ	Sequence 69 AA:
	Query Match 95.0% Score 344; DB 20; Length 69;
	Best Local Similarity 97.0%; Pred. No. 4.8e-38;
	Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	1 KGVSYRYPCRPFPESHAVANVKHLTLTPNCALOIVARLKNRRVCIDPKLKWIQE 60
Dd	2 KPVSLSIRKCPREFESHAVANVKHKLTLTPNCALOIVARLKNRRVCIDPKLKWIQE 61
OY	61 YLEKALN 67
Dd	62 YLEKALN 68
RESULT 13	
AAM50762	. . . . .
ID	AAM50762 standard; peptide: 72 AA.
AC	AAM50762:
XX	
DT	27-JUL-1998 (first entry)
DE	Peptide which binds to CXCR4 receptor and is useful for treating HIV.
XX	
KM	Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus; HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.

OS	XX	Homo sapiens.
XX	XX	FR2751658-A1.
PN	XX	30-JAN-1998.
PD	XX	26-JUL-1996; 96FR-0009477.
PF	XX	26-JUL-1996; 96FR-0009477.
XX	XX	26-JUL-1996; 96FR-0009477.
XX	XX	(INSP ) INST PASTEUR.
PA	XX	Arenzana SF, Baggiolini M, Clark LI, Moser B, Vitellizier JL;
PI	XX	WPI; 1998-123039/12.
DR	XX	Human stromal cell-derived chemokine, SDF-1 - useful for treating
PT	XX	human immunodeficiency virus infection
PT	XX	Claim 5; Page 29; 48pp; French.
PS	XX	The invention relates to peptides which bind to a cellular receptor for
CC	XX	CXC chemokines, namely the CXCR4 receptor (also known as leukocyte-
CC	XX	expressed transmembrane domain receptor), especially where the
CC	XX	peptide is human chemokine SDF-1. The peptide can be used to treat or
CC	XX	prevent HIV infections, optionally together with reverse transcriptase
CC	XX	inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4
CC	XX	receptor antagonists, immunotherapy agents, agents for treating HIV-
CC	XX	associated opportunistic infections and/or other CXC or CC chemokines,
CC	XX	especially RANTES, MIP-1 alpha, MIP-1 beta or MCP1. The peptide can be
CC	XX	used to detect anti-SDF-1 antibodies in biological fluids. This
CC	XX	sequence represents a specifically claimed peptide which binds to the
CC	XX	CXCR4 receptor.
XX	XX	Sequence 72 AA:
SO	XX	Query Match 95.0%; Score 344; DB 19; Length 72;
	XX	Best Local Similarity 97.0%; Pred. No. 5,1e-38;
	XX	Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1	KGVSPTSRPCRFESHVARANVHKLTLPNCALQIVARLKNRRVOCIDPKLWIO 60
DB	1	KPVLSYRCPCRPFESHVARANVHKLTLPNCALQIVARLKNRRVOCIDPKLWIO 60
QY	61	YLEKALN 67
DB	61	YLEKALN 67
RESULT 14		
ID	AAV34093	
AAV34093		standard; protein; 72 AA.
XX	AAV34093;	
AC	XX	29-NOV-1999 (first entry)
DT	XX	Native stromal cell derived factor 1 (SDF-1) beta protein.
XX	XX	
DE	XX	CXC chemokine receptor 4; CXCR4; antagonist; medicament; T-cell;
KW	XX	interferon gamma; autoimmune disease; multiple sclerosis; cancer;
KM	XX	angiogenesis; stromal cell derived factor 1; SDF-1.
OS	XX	Mammalia.
XX	XX	WO9947158-A2.
PN	XX	23-SEP-1999.
PD	XX	12-MAR-1999; 99WO-CAN00221.
PF	XX	13-MAR-1998; 98CA-2226391.

PR 14-AUG-1998; 98CA-2245224.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX  
 PI Clark-Lewis I, Gong J, Duronio V;  
 XX  
 DR WPI; 1999-561857/47.  
 XX  
 PT use of CXCR4 chemokine receptor 4 for treating autoimmune disease and  
 PT cancer -  
 XX  
 XX Example 1; Fig 1; 71pp; English.  
 PS  
 CC The invention relates to the use of a CXCR4 chemokine receptor 4 (CXCR4)  
 CC antagonist for the manufacture of a medicament for reducing interferon  
 CC gamma production by T-cells in a mammal. The CXCR4 antagonist can be used  
 CC to treat or to design a medicament to treat, an autoimmune disease,  
 CC multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4  
 CC antagonists may be peptide compounds comprising a substantially purified  
 CC peptide fragment, analogue or a pharmacologically acceptable salt of  
 CC stromal cell derived factor 1 (SDF-1). The present sequence represents  
 CC the amino acid sequence of SDF-1 beta protein.  
 XX  
 SQ Sequence 72 AA;  
 Query Match 95.0%; Score 344; DB 20; Length 72;  
 Best local similarity 97.0%; Pred. No. 5,1e-38;  
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 KGVSPSYRCPCRFESHVARANYKHILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 DB 1 KPVSLSYRCPCRFESHVARANYKHILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 QY 61 YLEKALN 67  
 DB 61 YLEKALN 67  
 RESULT 15  
 AA67595  
 ID AA67595 standard; peptide; 72 AA.  
 XX  
 AC AA67595;  
 XX  
 DT 13-JUN-2000 (first entry)  
 XX  
 DE SDF-1beta peptide sequence.  
 XX  
 XX SDF-1; CXCR4; CXCR4 chemokine receptor 4; gamma-interferon; cancer; gout;  
 KW autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;  
 KW type 1 diabetes; ulcerative colitis; lupus; antagonist; antitumor;  
 XX stromal cell derived factor one; anti-inflammatory; immunomodulatory.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200009152-A1.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 16-AUG-1999; 99WO-CA00750.  
 XX  
 PR 14-AUG-1998; 98CA-2245224.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX  
 PI Clark-Lewis I, Gong J, Duronio V, Salari H;  
 XX  
 DR WPI; 2000-224175/19.  
 XX  
 PT Therapeutic composition containing CXCR4 antagonist, useful for  
 PT treating autoimmune disease, especially multiple sclerosis and cancer  
 XX

PS Disclosure; Fig 1; 88pp; English.  
 XX  
 CC The invention provides a therapeutic composition containing an antagonist  
 CC of CXCR4 (CXCR4 chemokine receptor 4) and an excipient. The compositions  
 CC are specifically used: to reduce production of gamma-interferon by T  
 CC cells, particularly for treating autoimmune disease, especially multiple  
 CC sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral  
 CC sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative  
 CC colitis, gout, lupus and transplant rejection; to treat cancer by  
 CC inhibiting angiogenesis; inhibition of restenosis; and when labeled, to  
 CC evaluate in vivo pharmacokinetics, or to determine disease progression  
 CC and susceptibility, or as targeting agents for delivery of other  
 CC therapeutic agents. The antagonist is selected from SDF-1 (stromal cell  
 CC derived factor one) peptide fragments, SDF-1 being the only known natural  
 CC peptide sequence.  
 XX  
 SQ Sequence 72 AA;  
 Query Match 95.0%; Score 344; DB 21; Length 72;  
 Best local similarity 97.0%; Pred. No. 5,1e-38;  
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 KGVSPSYRCPCRFESHVARANYKHILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 DB 1 KPVSLSYRCPCRFESHVARANYKHILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 QY 61 YLEKALN 67  
 DB 61 YLEKALN 67

Search completed: January 23, 2003, 15:33:42  
 Job time : 29.2 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 23, 2003, 15:33:47 : Search time 9.8 Seconds  
(without alignments)  
201.157 Million cell updates/sec

Title: US-09-852-424-2

Perfect score: 362

Sequence: 1 KGVSPSYRCPCRFESHVAR.....QVCIDPKLKWIELEKALN 67

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents-AA:  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	344	95.0	89	1	US-08-323-084A-1
2	344	95.0	89	1	US-08-674-008-1
3	344	95.0	93	1	US-08-323-084A-5
4	344	95.0	93	1	US-08-674-008-5
5	344	95.0	326	3	US-08-808-720-3
6	344	95.0	328	3	US-08-808-720-1
7	343	94.8	89	1	US-08-181-556-2
8	94.5	26.1	70	1	US-08-330-163-24
9	94.5	26.1	70	1	US-08-482-111-24
10	94	26.0	67	1	US-08-244-702-12
11	94	26.0	67	1	US-08-244-702-14
12	94	26.0	68	1	US-08-244-702-9
13	94	26.0	68	1	US-08-244-702-10
14	94	26.0	68	1	US-08-244-702-11
15	94	26.0	69	1	US-08-244-702-2
16	94	26.0	69	1	US-08-244-702-8
17	94	26.0	72	1	US-07-956-863-1
18	94	26.0	72	1	US-07-778-413E-16
19	94	26.0	72	1	US-08-340-102-16
20	94	26.0	72	1	US-08-330-163-1
21	94	26.0	72	1	US-08-244-702-1
22	94	26.0	72	1	US-08-482-111-1
23	94	26.0	72	1	US-08-202-989-1
24	94	26.0	72	5	PCT-US94-02051-1
25	94	26.0	73	1	US-08-482-111-69
26	94	26.0	73	4	US-09-384-302A-26
27	94	26.0	76	2	US-08-468-819-79

28	94	26.0	76	2	US-08-468-819-81	Sequence 81, Appl
29	94	26.0	79	2	US-08-436-420-25	Sequence 25, Appl
30	94	26.0	99	1	US-08-352-324A-6	Sequence 6, Appl
31	94	26.0	99	2	US-08-862-607-6	Sequence 6, Appl
32	94	26.0	99	2	US-08-468-819-3	Sequence 3, Appl
33	94	26.0	99	3	US-09-203-235-6	Sequence 6, Appl
34	94	26.0	99	4	US-08-679-493A-150	Sequence 150, App
35	94	26.0	99	5	PCT-US95-16144-6	Sequence 6, Appl
36	94	26.0	99	6	5451399-2	Patent No. 5451399
37	92.5	25.6	72	3	US-08-846-966-1	Sequence 1, Appl
38	92.5	25.6	72	3	US-08-557-142-1	Sequence 1, Appl
39	92.5	25.6	72	4	US-09-467-160-1	Sequence 1, Appl
40	92.5	25.6	72	4	US-09-513-153-1	Sequence 1, Appl
41	92.5	25.6	72	4	US-09-467-155-1	Sequence 1, Appl
42	92.5	25.6	72	5	PCT-US94-06264-1	Sequence 1, Appl
43	92.5	25.6	77	2	US-08-436-420-41	Sequence 41, Appl
44	92	25.4	64	1	US-08-330-163-21	Sequence 21, Appl
45	92	25.4	64	1	US-08-482-111-21	Sequence 21, Appl

## ALIGNMENTS

```

RESULT 1
US-08-323-084A-1
; Sequence 1, Application US/08323084A
; Patent No. 5563048
; GENERAL INFORMATION:
; APPLICANT: HONJO, TASUKU
; APPLICANT: SHIROZU, MICHIO
; APPLICANT: TADA, HIDEAKI
; TITLE OF INVENTION: No. 5563048el Polypeptides and DNAs encoding them
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSSEE: SUGHRUE, MIOM, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,084A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 280505/1993
; FILING DATE: 14-OCT-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-323-084A-1

Query Match          95.0%; Score 344; DB 1; Length 89;
Best Local Similarity 97.0%; Pred. No. 1.9e-37;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 KGVSPSYRCPCRFESHVARAAVANKHKLITWPCALQIVARLKNRRNROVCIIDPKLWIOE 60
DB 22 KGVSPSYRCPCRFESHVARAAVANKHKLITWPCALQIVARLKNRRNROVCIIDPKLWIOE 81
QY 61 YLEKALN 67

```







US-08-482-111-24

Query Match	26.1%;	Score 94.5;	DB 1;	Length 70;
Best Local Similarity	32.8%;	Pred. No. 3.2e-05;		
Matches 20; Conservative	17;	Mismatches 21;	Indels 3;	Gaps 3;

Oy 8 RCPREFEESHVARANKHLKILNT-PNC-ALQIVARLKNRRVQCIDPKLKWIDEYLEKA 65  
::| | ::||: ||:||:|||| |: :  
Db 9 QCLCVKTTSOVRPRHITSLEVIAGPHCPTAQLIATLK-NGRKLCDPEKENMVAKIIKKL 67

Qy	66	L	66
		1	
Db	68	L	68

```

: RESULT 10
: US-08-244-702-12
: Sequence 12, Application US/08244702
: Patent No. 5665346
:
: GENERAL INFORMATION:
: APPLICANT: Clark-Lewis, Ian
: APPLICANT: Moser, Bernhard
: TITLE OF INVENTION: Human Interleukin-8 Analogs
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Morrison & Foerster
: STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20006-1812
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
:
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/244,702
: FILING DATE: 27-SEP-1994
: CLASSIFICATION: 424
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: FCT/CA92/00528
: FILING DATE: 03-DEC-1992
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/801,578
: FILING DATE: 04-DEC-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Murashige, Kate H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 8080-0004,20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 67 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
:
: US-08-244-702-12

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Query Match	26.0%	Score 94;	DB 1;	Length 67;
Best Local Similarity	32.3%;	Pred. No. 3.5e-05;		
Matches	20;	Conservative 18;	Mismatches 20;	Indels 4; Gaps 4;
Oy	8	RCPC-RPFESHVARANVHKLILNT-PNCA-LQIVARLKNNNROYCIPRKLWIOEYLEK	64	
	:	: :   : : :   :   :	: :   :           :	:
Db	1	RCOCITYSKRPHPKFIFELRVIESGPPHCANTETIYVL-SDGRELCLDPKENMVORVEK	59	
Oy	65	AL	66	
	-			
Db	60	FL	61	

RESULT 11  
US-08-244-702-14

Sequence 14, Application US/08244702  
 Patent No. 5655346  
 GENERAL INFORMATION:  
 APPLICANT: Clark-Lewis, Ian  
 APPLICANT: Moser, Bernhard  
 TITLE OF INVENTION: Human Interleukin-8 Analogs  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Morrison & Foerster  
 STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500  
 CITY: Washington

Query Match	26.08	Score	94	DB	1	Length	67
Best Local Similarity	32.38	Pred. NO.	3.5e-05				
Matches	20	Conservative	18	Mismatches	20	Indels	4
						Gaps	4

OY 8 RCPC-REFESHVARANVKILKILNT -PCA-LQIYAARKNNROVCDPLTKMIOEYLEK 64  
|| : : || : : || : : || : : || : : || : : || : : || : : || : : || : :  
Db 4 RQCCKITYSFPIPKRIKELRVIESGPHCANTEIVKL-SGRRLCLDPRENNVAQRVLEK 62

OY 65 AL 66  
|  
Db 63 FL 64

RESULT 12 702-9  
US-08-244-702-9  
Sequence 9, Application US/08244702  
Patent No. 5665346  
GENERAL INFORMATION:  
APPLICANT: Clark-Lewis, Ian  
APPLICANT: Moser, Bernhard  
TITLE OF INVENTION: Human Interleukin-8 Analogs  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrilson & Foerster  
STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.

ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/244,702  
FILING DATE: 27-SEP-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/CA92/00528  
FILING DATE: 03-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,578  
FILING DATE: 04-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 8080-0004.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-244-702-9

Query Match 26.0%; Score 94; DB 1; Length 68;  
Best Local Similarity 32.3%; Pred. No. 3.6e-05;  
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

QY 8 RCPC-REFRESHVARANVHKILINT-PNCA-DOIVARLNKNNQVCIIDPRKWIQYELK 64  
DB 2 RQCICITYSKPHRPKIKELRVIESGPHCANTEIYKL-SDGRELCIDPRENNVQRYVEK 60  
QY 65 AL 66  
DB 61 FL 62

RESULT 13  
US-08-244-702-10  
Sequence 10, Application US/08244702  
Patent No. 5665346  
GENERAL INFORMATION:  
APPLICANT: Clark-Lewis, Ian  
APPLICANT: Moser, Bernhard  
TITLE OF INVENTION: Human Interleukin-8 Analogs  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/244,702  
FILING DATE: 27-SEP-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/CA92/00528  
FILING DATE: 03-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,578

FILING DATE: 04-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 8080-0004.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-244-702-10

Query Match 26.0%; Score 94; DB 1; Length 68;  
Best Local Similarity 32.3%; Pred. No. 3.6e-05;  
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

QY 8 RCPC-REFRESHVARANVHKILINT-PNCA-DOIVARLNKNNQVCIIDPRKWIQYELK 64  
DB 2 RQCICITYSKPHRPKIKELRVIESGPHCANTEIYKL-SDGRELCIDPRENNVQRYVEK 60  
QY 65 AL 66  
DB 61 FL 62

RESULT 14  
US-08-244-702-11  
Sequence 11, Application US/08244702  
Patent No. 5665346

GENERAL INFORMATION:  
APPLICANT: Clark-Lewis, Ian  
APPLICANT: Moser, Bernhard  
TITLE OF INVENTION: Human Interleukin-8 Analogs  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/244,702  
FILING DATE: 27-SEP-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/CA92/00528  
FILING DATE: 03-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,578  
FILING DATE: 04-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 8080-0004.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-244-702-11



Query Match	26.0%	Score 94;	DB 1;	Length 68;
Best Local Similarity	32.3%	Pred. NO. 3.6e-05;		
Matches	20;	Conservative	18;	Mismatches 20;
			Indels	4;
			Gaps	4;

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0y      8 RCPC-RFEESHVARANKHLKILNT-PNCA-LQIVARLKNNRQVCIDPKLKWIOEYLEK 64
          |||::: :||:::||||: :||:::||||| |::: ||
Db     2 RQCICKTYSRPFHPFKIKELRVIESGPHCANTEIIVKL-SQGRCLCPKENMYGVREVK 60
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Qy	65	AL	66
		1	
Db	61	FL	62

RESULT 15  
US-08-244-702-2

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GENERAL INFORMATION:
APPLICANT: Clark-Lewis, Ian
APPLICANT: Moser, Bernhard
TITLE OF INVENTION: Human Interleukin-8 Analogs
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,702
FILING DATE: 27-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA92/00528
FILING DATE: 03-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,578
FILING DATE: 04-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 8080-0004.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
TYPE: amino acid
TOPOLOGY: linear

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Query Match	26.0%	Score 94	DB 1	Length 69
Best Local Similarity	32.3%	Pred. No.	3.6e-05	
Matches	20	Conservative	18	Mismatches 20
				Indels 4
				Gaps 4

Dy 8 RCPK-RFEESHVARANKVHLKIINT-PNCA-LQIVARLKNNNROYCIDPKLKWIEYLEK 64  
|| : : || :: : || : : || : : || : : ||  
Db 3 RCQCITKYSKPFPHPKFIKELRVIESGPHCANTEIILVKL-SDCRELCIDPENWYGRVEK 61

QY	65	AL	66
		1	
Db	62	FL	63

Search completed: January 23, 2003, 15:38:57  
Job time : 9.8 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:31:18 ; Search time 6.2 seconds  
(without alignments)  
218.059 Million cell updates/sec

Title: US-09-852-424-2

Perfect score: 362

Sequence: 1 KGVSPSYRCPCRFESHVAR.....QVCIDPKLKIOWLEKALN 67

Scoring table:

BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCRT\_NEW\_PUB pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCRTUS\_PUBCOMB pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	362	100.0	67	9	US-09-852-424-2
2	353	97.5	67	9	US-09-852-424-6
3	352	97.2	67	9	US-09-852-424-1
4	348	96.1	67	9	US-09-852-424-7
5	347	95.9	67	9	US-09-852-424-3
6	346	95.6	67	9	US-09-852-424-9
7	345	95.3	67	9	US-09-852-424-5
8	344	95.0	67	9	US-09-852-424-8
9	344	95.0	67	9	US-09-852-107-1
10	344	95.0	67	10	US-09-144-838-8
11	344	95.0	67	10	US-09-144-838-23
12	344	95.0	89	8	US-08-927-939-22
13	344	95.0	89	9	US-09-792-793A-32
14	344	95.0	89	10	US-09-953-692-4
15	344	95.0	89	10	US-09-953-717-4
16	344	95.0	93	8	US-08-927-939-56
17	344	95.0	93	9	US-09-835-107-2
18	344	95.0	93	9	US-09-835-107-3
19	344	95.0	93	9	US-09-792-793A-93

20	344	95.0	93	10	US-09-144-838-7	Sequence 7, Appl
21	344	95.0	93	10	US-09-919-497-95	Sequence 95, Appl
22	344	95.0	320	9	US-09-792-793A-77	Sequence 77, Appl
23	344	95.0	322	9	US-09-792-793A-78	Sequence 78, Appl
24	344	95.0	327	9	US-09-792-793A-79	Sequence 79, Appl
25	342	94.5	67	9	US-09-852-424-4	Sequence 4, Appl
26	340.5	94.1	66	9	US-09-852-424-10	Sequence 10, Appl
27	330.5	91.3	66	9	US-09-852-424-11	Sequence 11, Appl
28	328.5	90.7	66	9	US-09-852-424-12	Sequence 12, Appl
29	325.5	90.2	66	10	US-09-144-838-27	Sequence 27, Appl
30	320	88.4	68	10	US-09-144-838-31	Sequence 31, Appl
31	304	84.0	67	10	US-09-144-838-47	Sequence 47, Appl
32	293	80.9	68	10	US-09-144-838-24	Sequence 24, Appl
33	290	80.1	67	10	US-09-144-838-25	Sequence 25, Appl
34	275.5	76.1	67	10	US-09-144-838-28	Sequence 28, Appl
35	269	74.3	69	10	US-09-144-838-52	Sequence 52, Appl
36	266	73.5	68	10	US-09-144-838-53	Sequence 53, Appl
37	253	69.9	68	10	US-09-144-838-48	Sequence 48, Appl
38	252.5	69.8	66	10	US-09-144-838-29	Sequence 29, Appl
39	250	69.1	67	10	US-09-144-838-49	Sequence 49, Appl
40	239	66.0	68	10	US-09-144-838-26	Sequence 26, Appl
41	221.5	61.2	67	10	US-09-144-838-30	Sequence 30, Appl
42	221	61.0	67	10	US-09-144-838-31	Sequence 31, Appl
43	215	59.4	69	10	US-09-144-838-54	Sequence 54, Appl
44	210.5	58.1	66	10	US-09-144-838-35	Sequence 35, Appl
45	199	55.0	68	10	US-09-144-838-50	Sequence 50, Appl

#### ALIGNMENTS

RESULT 1  
US-09-852-424-2  
Sequence 2, Application US/09852424  
Patent No. US20020156034A1  
GENERAL INFORMATION:  
APPLICANT: The University of British Columbia; and  
TITLE OF INVENTION: CACRA ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: 80021-257  
CURRENT APPLICATION NUMBER: US/09/852,424  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: CA 2,305,787  
PRIOR FILING DATE: 2000-05-09  
PRIOR APPLICATION NUMBER: US 60/205,467  
NUMBER OF SEQ ID NOS: 135  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
US-09-852-424-2  
Query Match  
Best Local Similarity 100.0%; Score 362; Length 67;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KGVSPSYRCPCRFESHVARAVKHILINTPRCAQIYARLKNNNROVCIDPKLWIDE 60  
DB 1 KGVSPSYRCPCRFESHVARAVKHILINTPRCAQIYARLKNNNROVCIDPKLWIDE 60  
QY 61 YLEKALN 67  
DB 61 YLEKALN 67  
RESULT 2  
US-09-852-424-6  
Sequence 6, Application US/09852424

```
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (5)
; OTHER INFORMATION: Xaa=P*-proline-amino acid chimera. See page 17 of
; OTHER INFORMATION: disclosure for possible structures for P*
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; US-09-852-424-6
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Query Match 97.5%; Score 353; DB 9; Length 67;

Best Local Similarity 98.5%; Pred. No. 1,4e-32; Mismatches 1; Indels 0; Gaps 0;

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QY 1 KGVSPTXRCPCRFESHVARANKHLKILNTPMCAIQIYARLKNNNRQVCIDPKLKWIOE 60
DB 1 KGVSXSVRCPCRFESHVARANKHLKILNTPMCAIQIYARLKNNNRQVCIDPKLKWIOE 60
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QY 61 YLEKALN 67
DB 61 YLEKALN 67
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RESULT 3

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; US-09-852-424-1
; Sequence 1, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
; US-09-852-424-1
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Query Match 97.2%; Score 352; DB 9; Length 67;

Best Local Similarity 98.5%; Pred. No. 1,4e-32; Mismatches 1; Indels 0; Gaps 0;

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QY 1 KGVSPTXRCPCRFESHVARANKHLKILNTPMCAIQIYARLKNNNRQVCIDPKLKWIOE 60
DB 1 KGVSLSYRCPCRFESHVARANKHLKILNTPMCAIQIYARLKNNNRQVCIDPKLKWIOE 60
```

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QY 61 YLEKALN 67
DB 61 YLEKALN 67
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RESULT 4

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; US-09-852-424-7
; Sequence 7, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (6)
; OTHER INFORMATION: Xaa=P*-proline-amino acid chimera. See page 17 of
; OTHER INFORMATION: disclosure for possible structures for P*
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; US-09-852-424-7
```

Query Match 96.1%; Score 348; DB 9; Length 67;

Best Local Similarity 97.0%; Pred. No. 4e-32; Mismatches 2; Indels 0; Gaps 0;

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QY 1 KGVSPTXRCPCRFESHVARANKHLKILNTPMCAIQIYARLKNNNRQVCIDPKLKWIOE 60
DB 1 KGVSLSYRCPCRFESHVARANKHLKILNTPMCAIQIYARLKNNNRQVCIDPKLKWIOE 60
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```
QY 61 YLEKALN 67
DB 61 YLEKALN 67
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RESULT 5

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; US-09-852-424-3
; Sequence 3, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
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US-09-852-424-3

Query Match 95.9%; Score 347; DB 9; Length 67;  
Best Local Similarity 97.0%; Pred. No. 5.1e-32;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
DB 1 KGVSLYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67  
DB 61 YLEKALN 67

RESULT 6  
US-09-852-424-9

; Sequence 9, Application US/09852424  
; Patent No. US20020156034A1

; GENERAL INFORMATION:  
; APPLICANT: The University of British Columbia; and  
; APPLICANT: Chemokine Therapeutics Corporation  
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
; FILE REFERENCE: 80021-257  
; CURRENT APPLICATION NUMBER: US/09/852,424  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: CA 2,305,787  
; PRIOR FILING DATE: 2000-05-09  
; PRIOR APPLICATION NUMBER: US 60/205,467  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 9

; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MUTAGEN  
; LOCATION: (8)  
; OTHER INFORMATION: Xaa=P\*-proline-amino acid chimera. See page 17 of  
; OTHER INFORMATION: disclosure for possible structures for P\*  
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
; OTHER INFORMATION: Laboratory  
US-09-852-424-9

Query Match 95.6%; Score 346; DB 9; Length 67;  
Best Local Similarity 97.0%; Pred. No. 6.6e-32;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
DB 1 KGVSLYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67  
DB 61 YLEKALN 67

RESULT 7  
US-09-852-424-5

; Sequence 5, Application US/09852424  
; Patent No. US20020156034A1

; GENERAL INFORMATION:  
; APPLICANT: The University of British Columbia; and  
; APPLICANT: Chemokine Therapeutics Corporation  
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
; FILE REFERENCE: 80021-257  
; CURRENT APPLICATION NUMBER: US/09/852,424  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: CA 2,305,787  
; PRIOR FILING DATE: 2000-05-09  
; PRIOR APPLICATION NUMBER: US 60/205,467  
; PRIOR FILING DATE: 2000-05-19

; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5

; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
; OTHER INFORMATION: Laboratory  
US-09-852-424-5

Query Match 95.3%; Score 345; DB 9; Length 67;  
Best Local Similarity 97.0%; Pred. No. 8.5e-32;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
DB 1 KGVSLYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67  
DB 61 YLEKALN 67

RESULT 8  
US-09-852-424-8

; Sequence 8, Application US/09852424  
; Patent No. US20020156034A1

; GENERAL INFORMATION:  
; APPLICANT: The University of British Columbia; and  
; APPLICANT: Chemokine Therapeutics Corporation  
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
; FILE REFERENCE: 80021-257  
; CURRENT APPLICATION NUMBER: US/09/852,424  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: CA 2,305,787  
; PRIOR FILING DATE: 2000-05-09  
; PRIOR APPLICATION NUMBER: US 60/205,467  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8

; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MUTAGEN  
; LOCATION: (7)

; OTHER INFORMATION: Xaa=P\*-proline-amino acid chimera. See page 17 of  
; OTHER INFORMATION: disclosure for possible structures for P\*  
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
; OTHER INFORMATION: Laboratory  
US-09-852-424-8

Query Match 95.0%; Score 344; DB 9; Length 67;  
Best Local Similarity 97.0%; Pred. No. 1.1e-31;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
DB 1 KGVSLYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67  
DB 61 YLEKALN 67

RESULT 9  
US-09-835-107-1

; Sequence 1, Application US/09835107  
; Patent No. US20020165123A1  
; GENERAL INFORMATION:  
; APPLICANT: Tudan, Christopher R.

APPLICANT: Merzouk, Ahmed  
APPLICANT: Arab, Lakhdar  
APPLICANT: Saxena, Geeta  
APPLICANT: Bayes, Connie J.  
APPLICANT: Cashman, Johanne  
APPLICANT: Clark-Lewis  
APPLICANT: Saliari, Hassan  
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: SMAR012  
CURRENT APPLICATION NUMBER: US/09/835,107  
CURRENT FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: CA 2,305,036  
PRIOR FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: US 60/232,425  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: CA 2,335,109  
PRIOR FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 1  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: SDF-1 alpha  
US-09-835-107-1

Query Match 95.0%; Score 344; DB 9; Length 67;  
Best Local Similarity 97.0%; Pred. No. 1,1e-31;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSPSYRCPCRFESHVARANVHKILNTPNCAIOIVARLKNNNQVCIDPKLKWIOE 60  
Db 1 KPVSLSTRCPREFESHVARANVHKILNTPNCAIOIVARLKNNNQVCIDPKLKWIOE 60  
QY 61 YLEKALN 67  
Db 61 YLEKALN 67  
RESULT 10  
US-09-144-838-8  
Sequence 8, Application US/09144838A  
Patent No. US20020051996A1  
GENERAL INFORMATION:  
APPLICANT: Siani, Michael A.  
APPLICANT: Wilken, Jill  
APPLICANT: Simon, Reyna  
APPLICANT: Kent, Stephen B.H.  
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation  
FILE REFERENCE: GREN-020/01US  
CURRENT APPLICATION NUMBER: US/09/144,838A  
CURRENT FILING DATE: 1998-08-31  
EARLIER APPLICATION NUMBER: US 60/057,620  
EARLIER FILING DATE: 1997-09-04  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 8  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-144-838-8

Query Match 95.0%; Score 344; DB 10; Length 67;  
Best Local Similarity 97.0%; Pred. No. 1,1e-31;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 KGVSPSYRCPCRFESHVARANVHKILNTPNCAIOIVARLKNNNQVCIDPKLKWIOE 60  
Db 1 KPVSLSTRCPREFESHVARANVHKILNTPNCAIOIVARLKNNNQVCIDPKLKWIOE 60

QY 61 YLEKALN 67  
Db 61 YLEKALN 67  
RESULT 11  
US-09-144-838-23  
Sequence 23, Application US/09144838A  
Patent No. US20020051996A1  
GENERAL INFORMATION:  
APPLICANT: Siani, Michael A.  
APPLICANT: Wilken, Jill  
APPLICANT: Simon, Reyna  
APPLICANT: Kent, Stephen B.H.  
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation  
FILE REFERENCE: GREN-020/01US  
CURRENT APPLICATION NUMBER: US/09/144,838A  
CURRENT FILING DATE: 1998-08-31  
EARLIER APPLICATION NUMBER: US 60/057,620  
EARLIER FILING DATE: 1997-09-04  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 23  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-144-838-23

Query Match 95.0%; Score 344; DB 10; Length 67;  
Best Local Similarity 97.0%; Pred. No. 1,1e-31;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSPSYRCPCRFESHVARANVHKILNTPNCAIOIVARLKNNNQVCIDPKLKWIOE 60  
Db 1 KPVSLSTRCPREFESHVARANVHKILNTPNCAIOIVARLKNNNQVCIDPKLKWIOE 60  
QY 61 YLEKALN 67  
Db 61 YLEKALN 67  
RESULT 12  
US-08-927-939-22  
Sequence 22, Application US/08927939  
Patent No. US20010006640A1  
GENERAL INFORMATION:  
APPLICANT: Grainger, David J.  
APPLICANT: Tatalick, Lauen Marie  
TITLE OF INVENTION: Compounds and methods to inhibit or  
FILE REFERENCE: 295.022US1  
CURRENT APPLICATION NUMBER: US/08/927,939  
CURRENT FILING DATE: 1997-09-11  
NUMBER OF SEQ ID NOS: 83  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 22  
LENGTH: 89  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-08-927-939-22

Query Match 95.0%; Score 344; DB 8; Length 89;  
Best Local Similarity 97.0%; Pred. No. 1,4e-31;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 KGVSPSYRCPCRFESHVARANVHKILNTPNCAIOIVARLKNNNQVCIDPKLKWIOE 60  
Db 22 KPVSLSTRCPREFESHVARANVHKILNTPNCAIOIVARLKNNNQVCIDPKLKWIOE 81  
QY 61 YLEKALN 67  
Db 61 YLEKALN 67







GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: January 23, 2003, 15:31:02 : Search time 11.6 Seconds  
(Without alignments) 555.259 Million cell updates/sec

Title: US-09-852-424-2

Perfect score: 362  
Sequence: 1 KGVSPSYRCPCRFESHVAR.....OVCIDPKLKWIOEYLEKALN 67

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	344	95.0	93	2	G01540
2	343	94.8	89	2	A53497
3	343	94.8	89	2	I53416
4	343	94.8	93	2	I81182
5	101	27.9	101	2	I48148
6	99	27.3	95	2	JN0841
7	94	26.0	99	2	A37034
8	93	25.7	101	2	S42496
9	92.5	25.6	96	2	A32954
10	92	25.4	103	2	A53096
11	90.5	25.0	91	1	A46539
12	89.5	24.7	96	2	JN0572
13	88	24.3	101	2	I46871
14	88	24.3	120	2	I48147
15	86.5	23.9	100	2	JH0200
16	85.5	23.6	91	1	A28815
17	85	23.5	109	2	A54678
18	82.5	22.8	75	2	A54188
19	81.5	22.5	75	2	B54188
20	81.5	22.5	92	2	I52322
21	81.5	22.5	100	2	I51467
22	81.5	22.5	100	2	I55614
23	81.5	22.5	119	2	S42881
24	81.5	22.5	120	2	JE0177
25	81	22.4	148	1	A30209
26	81	22.4	148	1	S07723
27	79.5	22.0	101	2	B28414
28	79.5	22.0	107	2	B38250
29	79.5	22.0	107	2	A28414

30	78.5	21.7	132	2	A57325
31	77.5	21.4	114	2	A55010
32	77.5	21.4	117	2	B44253
33	76.5	21.1	103	2	A26736
34	76.5	21.1	103	2	I50417
35	74.5	20.6	96	2	I48099
36	73.5	20.3	107	2	JH0281
37	72.5	20.0	126	2	A35766
38	72.5	20.0	870	2	A41130
39	72	19.9	92	2	A32393
40	72	19.9	96	2	JC2478
41	71.5	19.8	128	1	TGHU
42	70.5	19.5	53	2	I64831
43	70.5	19.5	90	2	S69133
44	69.5	19.2	104	1	PFR04A
45	69	19.1	93	2	B35673

## ALIGNMENTS

## RESULT 1

G01540

Cytokine SDF-1-beta - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 26-Aug-1999

C:Accession: G01540

R:Spotila, L.D.

submitted to the EMBL Data Library, October 1994

A:Reference number: G07697

A:Accession: G01540

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-93 <SPO>

A:Cross-references: EMBL:U16752; NID:91272194; PID:9571508

C:Superfamily: beta-thromboglobulin

Query Match

Best Local Similarity 95.0%; Score 344; DB 2; Length 93;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy	1	KGVSPSYRCPCRFESHVARANKHLKILNPNCALQIVARLKNNNROYCIDPKLWIOE 60
Db	22	KPVSLSTYRCPCRFESHVARANKHLKILNPNCALQIVARLKNNNROYCIDPKLWIOE 81
Oy	61	YLEKALN 67
Db	82	YLEKALN 88

RESULT 2

A53497

pre-B-cell growth-stimulating factor precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 20-Jun-2000

C:Accession: A53497; I59582

R:Nagasawa, T.; Kikutani, H.; Kishimoto, T.

Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994

A:Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.

A:Reference number: A53497; MUID:94181581; PMID:8134392

A:Accession: A53497

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-89 <NAG>

A:Cross-references: GB:D21072; NID:9413905; PID:BA04648.1; PID:9468457

R:Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T.

Science 261, 600-603, 1993

A:Title: Signal sequence tripp: a cloning strategy for secreted proteins and type I me

A:Reference number: I59582; MUID:93342488; PMID:8342023

A:Accession: I59582

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-89 <RES>

A:Cross-references: GB:L12029; NID:g9393179; PIDN:AAA40100.1; PID:g9393180  
 C:Genetics:  
 A:Gene: SDF-1-alpha  
 C:Superfamily: beta-thromboglobulin  
 C:Keywords: cytokine

Query Match 94.8%; Score 343; DB 2; Length 89;  
 Best Local Similarity 95.5%; Pred. No. 3.5e-35;  
 Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60  
 DB 22 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 81  
 OY 61 YLEKALN 67  
 DB 82 YLEKALN 88

RESULT 3

Interleukin-8 homolog - mouse

C:Species: Mus sp. (mouse)  
 C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
 C:Accession: I53416  
 R:Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.  
 Exp. Cell Res. 215, 284-293, 1994  
 A:Title: Molecular cloning of TPRL1, a gene whose expression is repressed by the tumor F

A:Accession: I53416  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-89 <RES>  
 A:Cross-references: GB:S74318; NID:g786393; PIDN:AAB32650.1; PID:g786394  
 C:Genetics:  
 A:Gene: TPRL1

C:Superfamily: beta-thromboglobulin

Query Match 94.8%; Score 343; DB 2; Length 89;  
 Best Local Similarity 95.5%; Pred. No. 3.5e-35;  
 Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60  
 DB 22 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 81  
 OY 61 YLEKALN 67  
 DB 82 YLEKALN 88

RESULT 4

Cytokine - mouse

C:Species: Mus musculus (house mouse)  
 C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
 C:Accession: I81182  
 R:Tashiro, K.; Tada, H.; Heliker, R.; Shirozu, M.; Nakano, T.; Honjo, T.  
 Science 261, 600-603, 1993  
 A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I membr

A:Reference number: I59582; MUID:93342488; PMID:8342023

A:Accession: I81182

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-93 <RES>

A:Cross-references: GB:L12030; NID:g9393181; PIDN:AAA40101.1; PID:g9393182

C:Genetics:

A:Gene: SDF-1-beta

C:Superfamily: beta-thromboglobulin

Query Match 94.8%; Score 343; DB 2; Length 93;  
 Best Local Similarity 95.5%; Pred. No. 3.6e-35;  
 Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSPSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60  
 DB 22 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 81

OY 61 YLEKALN 67  
 DB 82 YLEKALN 88

RESULT 5

Neutrophil attractant protein-1 - guinea pig

C:Species: Cavia porcellus (guinea pig)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Aug-1999  
 C:Accession: I48148  
 R:Yoshimura, T.; Johnson, D.G.  
 J. Immunol. 151, 6225-6236, 1993  
 A:Title: cDNA cloning and expression of guinea pig neutrophil attractant protein-1 (N

A:Reference number: I48148; MUID:94065176; PMID:7504015

A:Accession: I48148

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-101 <RES>

A:Cross-references: GB:L04986; NID:g459764; PIDN:AAA37049.1; PID:g459765

C:Genetics:

A:Gene: NAP-1

C:Superfamily: beta-thromboglobulin

Query Match 27.9%; Score 101; DB 2; Length 101;  
 Best Local Similarity 35.9%; Pred. No. 3.1e-05;  
 Matches 23; Conservative 16; Mismatches 17; Indels 8; Gaps 5;

OY 8 RCPDRFESHVARAN--VKHLKILNT-PNCA-LQIVARLKNNNROYCIDPKLKWIOEYL 62  
 DB 33 RQCC--IKHTTPHFKFKELKVLKESGPRCANSEITVRL-SDNRQLCDPKKKWYQDVV 89

OY 63 EKAL 66  
 DB 90 SMFL 93

RESULT 6

JN0841

Interleukin-8 - dog

C:Species: Canis lupus familiaris (dog)  
 C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 12-Apr-1995  
 C:Accession: JN0841  
 R:Shikawa, J.; Suzuki, S.; Hotta, K.; Hirota, Y.; Mizuno, S.; Suzuki, K.  
 Gene 131, 305-306, 1993  
 A:Title: Cloning of a canine gene homologous to the human interleukin-8-encoding gene

A:Reference number: JN0841; MUID:94010328; PMID:7916715

A:Accession: JN0841

A:Molecule type: DNA

A:Residues: 1-95 <TSH>

C:Comment: This protein is a polymorphonuclear leukocytes chemotactic factor and is 1

C:Genetics:

A:Introns: 22/1: 67/2

C:Superfamily: beta-thromboglobulin

Query Match 27.3%; Score 99; DB 2; Length 95;  
 Best Local Similarity 34.8%; Pred. No. 5.1e-05;  
 Matches 23; Conservative 15; Mismatches 20; Indels 8; Gaps 4;

OY 3 VSPSYRCPCRFESHVARANKHLKILNT---PNCA-LQIVARLKNNNROYCIDPKLKW 57  
 DB 28 VSELRCQC--IKHTSTPHPKYIKELRVIDSGPHCENSEIIVKLNGN-EVCLDPKEKW 84

OY 58 IOEYLE 63  
 DB 85 VQKVVQ 90



```

A:Molecule type: mRNA
A:Residues: 1-99 <RE2>
A:Cross-references: GB:M17017; NID:9179579; PIDN:AAA55611.1; PID:9179580
R:Kusner, D.J.; Luebers, E.L.; Nowinski, R.J.; Konieczkowski, M.; King, C.H.; Sedor, J.
Kidney Int. 39, 1240-1248, 1991
A:Title: Cytokine- and LPS-induced synthesis of interleukin-8 from human mesangial cells
A:Reference number: 137902; MUID:913474977; PMID:1895676
A:Accession: 137902
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-97 <RE3>
A:Cross-references: EMBL:Z1686; NID:933958; PIDN:CAA77745.1; PID:933959
R:Alouani, S.; Gaertner, H.F.; Wermud, J.J.; Power, C.A.; Bacon, K.B.; Wells, T.N.C.;
Eur. J. Biochem. 227, 328-334, 1995
A:Title: A fluorescent interleukin-8 receptor probe produced by targeted labelling at t
A:Reference number: S67519; MUID:95154308; PMID:7851404
A:Accession: S67519
A:Molecule type: mRNA
A:Residues: 1-99 <ALO>
C:Comment: This secretory protein is chemotactic for polymorphonuclear leukocytes.
C:Comment: This protein is variably processed at the amino end. The major form differs
C:Genetics:
A:Gene: GDB:IL8
A:Cross-references: GDB:120099; OMIM:146930
A:Map position: 4q13-4q21
A:Introns: 22/1; 67/2; 95/2
C:Superfamily: beta-thromboglobulin
C:Keywords: chemotaxis; cytokine; inflammation
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-99/Product: interleukin-8, minor form #status experimental <MAT>
F:23-99/Product: interleukin-8, major lymphocyte/monocyte-derived form #status experimen
F:28-99/Product: interleukin-8, major lymphocyte/monocyte-derived form #status experimen

Query Match 26.0%; Score 94; DB 2; Length 99;
Best Local Similarity 32.3%; Pred. No. 0.00022;
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

Qy 8 RCPCRFESHVARNVKHLKILNT-PNCA-LQIVARLKNNNRQVCIDPKLKWIOEYLEK 64
Db 33 RCQCITRYSRPFKPKFKELRVIESGPHCANTEIIVKL-SDGRELCLDPRENNVQVRVEK 91

Qy 65 AL 66
Db 92 FL 93

RESULT 8
S42496
Interleukin-8 precursor [similarity] - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 19-Jan-2001
C:Accession: S42496; I46997
R:Legssteel, I.; Greenland, T.; Arnaud, P.; Morne, J.F.; Cordier, G.
submitted to the EMBL Data Library, March 1994
A:Description: Nucleotide sequence of ovine interleukin 8 cDNA using polymerase chain re
A:Reference number: S42496
A:Accession: S42496
A:Molecule type: mRNA
A:Residues: 1-101 <LEG>
A:Cross-references: EMBL:X78306; NID:9463253; PIDN:CAA55115.1; PID:9463254
R:Seow, H.F.; Yoshimura, T.; Wood, P.R.; Colditz, I.G.
Immunol. Cell Biol. 72, 398-405, 1994
A:Title: Cloning, sequencing, expression and inflammatory activity in skin of ovine inte
A:Reference number: I46997; MUID:95137661; PMID:7835984
A:Accession: I46997
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-101 <SEO>
A:Cross-references: GB:S74436; NID:9786590; PIDN:AA833241.1; PID:9786591
C:Genetics:
A:Gene: IL-8
C:Superfamily: beta-thromboglobulin
C:Keywords: chemotaxis; cytokine; inflammation

```

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F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-101/Product: interleukin-8 #status predicted <MAT>

Query Match 25.7%; Score 93; DB 2; Length 101;
Best Local Similarity 30.4%; Pred. No. 0.0003;
Matches 21; Conservative 20; Mismatches 20; Indels 8; Gaps 5;

Qy 3 VSPSYRCPREFESHVARAN--VKHLKILNT-PNCA-LQIVARLKNNNRQVCIDPKLKW 57
Db 28 MSRELRCQC--IKTSTPFPKFKELRVIESGPHCANTEIIVKL-TNCKEVCIDPKKRW 84

Qy 58 IDEYLEKAL 66
Db 85 VQKVOAFL 93

RESULT 9
A32954
gro-alpha precursor - mouse
N:Alternate names: gro protein; growth regulated protein; melanoma growth-stimulating
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1989 #sequence_revision 20-Oct-1989 #text_change 20-Aug-1999
C:Accession: A32954; JH0081
R:Quigley, P.; Alberta, J.; Wen, D.; Graycar, J.L.; Derynck, R.; Stiles, C.D.
J. Biol. Chem. 264, 4133-4137, 1989
A:Title: The platelet-derived growth factor-inducible KC gene encodes a secretory pro
A:Reference number: A32954; MUID:89139485; PMID:2917992
A:Accession: A32954
A:Molecule type: mRNA
A:Residues: 1-96 <QOU>
A:Cross-references: GB:J04596; NID:9201042; PIDN:AAA40131.1; PID:9201043
R:Ryssek, R.P.; MacDonald-Bravo, H.; Mattei, M.G.; Bravo, R.
Exp. Cell Res. 180, 266-275, 1989
A:Title: Cloning and sequence of a secretory protein induced by growth factors in mou
A:Reference number: JH0081; MUID:89078502; PMID:2909392
A:Accession: JH0081
A:Molecule type: mRNA
A:Residues: 1-96 <RYS>
C:Comment: This protein is basic and lacks threonine, phenylalanine, and tyrosine.
C:Genetics:
A:Map position: 5
C:Superfamily: beta-thromboglobulin
C:Keywords: extracellular protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-96/Product: gro-alpha #status predicted <MAT>

Query Match 25.6%; Score 92.5; DB 2; Length 96;
Best Local Similarity 30.3%; Pred. No. 0.00033;
Matches 20; Conservative 19; Mismatches 24; Indels 3; Gaps 3;

Qy 3 VSPSYRCPREFESHVARNVKHLKIL-NTPNCA-LQIVARLKNNNRQVCIDPKLKWIOE 60
Db 27 IANELRCQCQLQTMAGHILKNISLAKVLPSPHCTQTEVATLTK-NGREACLDPEAPLVOK 85

Qy 61 YLEKAL 66
Db 86 IVQKML 91

RESULT 10
A53096
Interleukin-8 precursor - pig
N:Alternate names: alveolar macrophage chemotactic factor-I (MwCF-I)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 19-Jan-2001
C:Accession: A53096; A44253
R:Lin, G.; Pearson, A.E.; Scamurra, R.W.; Zhou, Y.; Baarsch, M.J.; Weiss, D.J.; Murta
J. Biol. Chem. 269, 77-85, 1994
A:Title: Regulation of interleukin-8 expression in porcine alveolar macrophages by ba
A:Reference number: A53096; MUID:94103307; PMID:8276881
A:Accession: A53096
A:Status: preliminary
A:Molecule type: mRNA

```



A:Accession: S51214  
 A:Molecule type: protein  
 A:Residues: 25-96 <HAN>  
 C:Comment: This protein has chemotactic activity for neutrophils and has melanoma growth  
 C:Genetics:  
 A:Gene: gro; KC  
 A:introns: 24/1; 65/2; 92/2  
 C:Superfamily: beta-thromboglobulin  
 C:Keywords: cytokine; disulfide bond  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-96/Product: neutrophil chemo-attractant gro protein #status experimental <CYT>

Query Match 24.7%; Score 89.5; DB 2; Length 96;  
 Best Local Similarity 30.3%; Pred. No. 0.00076;  
 Matches 20; Conservative 18; Mismatches 25; Indels 3; Gaps 3;

OY 3 VSPSYRCPCEFFESHVARANKHLKILNT-PNCA-LOIVARLKNNNQVCDPKLKIQE 60  
 Db 27 VANELRCQCLQTVAGIHFKNIQSLKMPGPCHQTEVIATLK-NGREACLDPEAPVVK 85

OY 61 YLEKAL 66  
 Db 86 IVCKML 91

# RESULT 13

146871  
 Interleukin-8 - rabbit  
 N:Alternate names: neutrophil attractant/activation protein-1

C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 20-Aug-1999

C:Accession: I46871; S13052  
 R:Yoshimura, T.; Yunhi, N.

J:Immunol. 146, 3483-3488, 1991  
 A:Title: Neutrophil attractant/activation protein-1 and monocyte chemoattractant protein

A:Reference number: I46857; MUID:91225489; PMID:2026877

A:Accession: I46871  
 A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA  
 A:Residues: 1-101 <YOS>

A:Cross-references: GB:M57439; NID:g165552; PIDN:AAA31422.1; PID:g165553

R:Beaudien, B.C.; Collins, P.D.; Jose, P.J.; Totty, N.F.; Hsuan, J.; Waterfield, M.D.; W  
 Blochem. J. 271, 797-801, 1990

A:Title: A novel neutrophil chemoattractant generated during an inflammatory reaction in  
 Interleukin 8.

A:Reference number: S13052; MUID:91058518; PMID:2244880

A:Accession: S13052  
 A:Molecule type: protein  
 A:Residues: 23-33, 'X', '35', 'X', '37-46', 'X', '48-49', 'T', '51-53 <BEA>

C:Superfamily: beta-thromboglobulin  
 C:Keywords: cytokine

Query Match 24.3%; Score 88; DB 2; Length 101;  
 Best Local Similarity 28.8%; Pred. No. 0.0012;  
 Matches 19; Conservative 21; Mismatches 18; Indels 8; Gaps 5;

OY 3 VSPSYRCPCEFFESHVARANKHLKILNT-PNCA-LOIVARLKNNNQVCDPKLKI 57  
 Db 28 IGTLEKRCQCL-IKTHSPHFHFKELRVIESGPHCANSELIIVLV-DGRELCIDPEKEM 84

OY 58 IOEYLE 63  
 Db 85 VOKVVO 90

RESULT 14  
 148147  
 monocyte chemoattractant protein-1 - guinea pig  
 C:Species: Cavia porcellus (guinea pig)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999

C:Accession: I48147  
 R:Yoshimura, T.  
 J:Immunol. 150, 5025-5032, 1993

A:Title: cDNA cloning of guinea pig monocyte chemoattractant protein-1 and expression  
 A:Reference number: I48147; MUID:93267104; PMID:8496603  
 A:Accession: I48147  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-120 <RES>  
 A:Cross-references: GB:L04985; NID:g349820; PIDN:AAA37047.1; PID:g349821  
 C:Genetics:  
 A:Gene: MCP-1  
 C:Superfamily: macrophage inflammatory protein

Query Match 24.3%; Score 88; DB 2; Length 120;  
 Best Local Similarity 29.6%; Pred. No. 0.0015;  
 Matches 16; Conservative 10; Mismatches 28; Indels 0; Gaps 0;

OY 11 CRFEESHVARANKHLKILNT-PNCA-LOIVARLKNNNQVCDPKLKI 64  
 Db 34 CYTFNKQIPLKRKVGERTTSSRCPEAVIFRLKNEVCADPTQKWDYIAK 87

# RESULT 15

JH0200  
 macrophage inflammatory protein 2 precursor - mouse

C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 20-Aug-1999

C:Accession: JH0200; A32190  
 R:Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; McClain, J.; Sherry, B.; Fabre, M.; van

J:Exp. Med. 172, 911-919, 1990  
 A:Title: Cloning and characterization of cDNAs for murine macrophage inflammatory pro

A:Reference number: JH0200; MUID:90354792; PMID:2201751

A:Accession: JH0200  
 A:Molecule type: mRNA

A:Residues: 1-100 <TEK>

A:Cross-references: GB:X53798; NID:g53128; PIDN:CA37807.1; PID:g53129

R:Moipe, S.D.; Sherry, B.; Juers, D.; Davatellis, G.; Yurt, R.W.; Cerami, A.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 612-616, 1989

A:Title: Identification and characterization of macrophage inflammatory protein 2.

A:Reference number: A32190; MUID:89098980; PMID:2643119

A:Accession: A32190  
 A:Molecule type: protein

A:Residues: 28-59 <WOL>

C:Superfamily: beta-thromboglobulin  
 C:Keywords: heparin binding

F:1-27/Domain: signal sequence #status predicted <SIG>  
 F:28-100/Product: macrophage inflammatory protein 2 #status experimental <MAT>

Query Match 23.9%; Score 86.5; DB 2; Length 100;  
 Best Local Similarity 30.0%; Pred. No. 0.0019;  
 Matches 21; Conservative 19; Mismatches 21; Indels 9; Gaps 4;

OY 3 VSPSYRCPCEFFESHVARANKHLKILNT-PNCA-LOIVARLKNNNQVCDPKLKI 57  
 Db 30 VASELRCQCL-KTLPRVDFKNIGSLSTPRPGHCAQTEVIATLK-GGKVCCLDEAPL 85

OY 58 IOEYLEKALN 67  
 Db 86 VOKIKQILN 95

Search completed: January 23, 2003, 15:37:24  
 Job time: 12.6 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 23, 2003, 15:28:07 ; Search time 6 Seconds

(without alignments)  
463.152 Million cell updates/sec

Title: US-09-852-424-2

Perfect score: 362  
Sequence: 1 KGVSPSYRCPCRFESHVAR.....QVCIDPKLKIQIEYLEKALN 67

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SWISSPROT\_40.\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	344	95.0	93	1 SDF1_FELCA	062657 felis silve
2	344	95.0	93	1 SDF1_HUMAN	P48061 homo sapien
3	343	94.8	89	1 SDF1_MOUSE	P40324 mus musculu
4	102	28.2	101	1 IL8_CANEA	P41324 canis famill
5	101	27.9	101	1 IL8_CAVPO	P49113 cavia porce
6	99	27.3	101	1 IL8_HUMAN	P09855 felis silve
7	94	26.0	99	1 IL8_HUMAN	P10145 h interleuk
8	93	25.7	101	1 IL8_SHEEP	P36925 ovis aries
9	92.5	25.6	96	1 GRO_MOUSE	P12850 mus musculu
10	92	25.4	103	1 IL8_PIG	P26894 sus scrofa
11	91	25.1	101	1 IL8_MACMU	P51495 macaca mula
12	90.5	25.0	91	1 SY05_MOUSE	P30882 mus musculu
13	90.5	25.0	91	1 SY05_MOUSE	P50231 ratu
14	90	24.9	101	1 IL8_BOVIN	P79255 bos taurus
15	90	24.9	130	1 SZ05_RAT	P97885 ratu
16	89.5	24.7	96	1 GRO_RAT	P14095 ratu
17	88	24.3	101	1 IL8_RABIT	P19874 orycto
18	88	24.3	120	1 SY02_CAVPO	Q08782 cavia porce
19	87.5	24.2	91	1 SY05_CAVPO	P97272 cavia porce
20	87	24.0	101	1 IL8_CERTO	P46653 cercocebu
21	86.5	23.9	100	1 MIR2_MOUSE	P10889 mus musculu
22	85.5	23.6	50	1 SY05_PIG	Q29288 sus scrofa
23	85.5	23.6	91	1 SY05_HUMAN	P13501 homo sapien
24	85	23.5	99	1 SY07_HUMAN	P80098 homo sapien
25	82.5	22.8	114	1 SZ06_HUMAN	P80162 homo sapien
26	81.5	22.5	71	1 GRO1_RABIT	P30782 orycto
27	81.5	22.5	92	1 SY03_RAT	P50229 ratu
28	81.5	22.5	100	1 MIR2_RAT	P30348 ratu
29	81.5	22.5	112	1 SZ06_BOVIN	P80221 bos taurus
30	81.5	22.5	119	1 SZ07_PIG	P43030 sus scrofa
31	81	22.4	148	1 SY02_MOUSE	P10148 mus musculu
32	81	22.4	148	1 SY02_RAT	P14644 ratu
33	80.5	22.2	120	1 SY16_HUMAN	O15467 h small ind

34	80	22.1	89	1 SY18_HUMAN	P55774 h small ind
35	79.5	22.0	101	1 GRO_CRIGR	P09340 cricetus
36	79.5	22.0	107	1 GRO_HUMAN	P09341 homo sapien
37	79.5	22.0	107	1 MIR2_HUMAN	P19876 homo sapien
38	78.5	21.7	91	1 SY05_BOVIN	O97919 bos taurus
39	78.5	21.7	132	1 SZ05_MOUSE	P50228 mus musculu
40	78	21.5	97	1 SY08_MOUSE	O92121 mus musculu
41	78	21.5	109	1 SZ13_HUMAN	O43927 homo sapien
42	77.5	21.4	114	1 SZ05_HUMAN	P42830 homo sapien
43	77.5	21.4	117	1 AMC2_PIG	P22952 sus scrofa
44	77	21.3	98	1 SY13_HUMAN	O99616 homo sapien
45	76.5	21.1	103	1 EMF1_CHICK	P08317 gallus gall

ALIGNMENTS

RESULT 1

ID SDF1\_FELCA STANDARD: PRT: 93 AA.

AC 062657; 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DE 15-JUN-2002 (Rel. 41, Last annotation update)

GN Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12).

OS SDF1.

OC Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OX NCBI\_Taxid=9685;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Thymus;

RA MEDLINE=98450506; PubMed=9777331;

RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiyama Y., Nakamura K.,

RA Cai J.S., Sato E., Kohmoto M., Mikami T.;

RT "Molecular cloning and sequencing of feline stromal cell-derived

RT factor-1 alpha and beta.";

RT Eur. J. Immunogenet. 23:303-305(1998).

RL -i- FUNCTION: CHEMOKINE-INDUCED T-LYMPHOCYTES, MONOCYTES, BUT

CC NOT NEUTROPHILS.

CC -i- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE);

CC ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -i- SIMILARITY: BELONGS TO THE INTERKINE ALPHA FAMILY (SMALL CYTOKINE

CC C-X-C) (CHEMOKINE CXC).

CC -----

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CC -----

CC DR EMBL: AB011966; BAA28602.1; -

CC DR HSPB: P48061; ISDP.

CC DR InterPro: IPR001089; CXC\_chemokine-sm11.

CC DR InterPro: IPR001811; Chemokine\_IL8.

CC DR Pfam: PF00048; IL8; 1.

CC DR SMART: SM00199; SCY; 1.

CC DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; FALSE\_NEG.

CC KW Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing;

CC FT SIGNAL 1 19

CC FT CHAIN 20 93 STROMAL CELL-DERIVED FACTOR 1.

CC FT DISULFID 30 55 BY SIMILARITY.

CC FT FT 32 71 BY SIMILARITY.

CC FT VARSPLIC 90 93 MISSING (IN ISOFORM ALPHA).

CC SQ SEQUENCE 93 AA; 10581 MM; 44FC7637119BEB37 CRC64;

Query Match Best Local Similarity 95.0%; Score 344; DB 1; Length 93;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;





RA Weinstein I.B. ;  
 RT "Molecular cloning of TPARI, a gene whose expression is repressed by  
 the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA).";  
 RL Exp. Cell Res. 215:284-293(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AKR/J;  
 RA Nomura M., Nakata Y., Uzuwa A., Nose M., Akashi M., Suzuki G. ;  
 RL Submitted (DEC-1994) to the EMBL/Genbank/DDJJ databases.  
 CC -1- FUNCTION: CHEMOTACTICANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT  
 NOT NEUTROPHILS.  
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF BONE MARROW-DERIVED B  
 PROGENITOR CELLS IN THE PRESENCE OF IL-7 AS WELL AS GROWTH OF THE  
 STROMAL CELL-DEPENDENT B-CELL CLONE DM34 CELLS.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE);  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE  
 C-X-C) (CHEMOKINE CXC).  
 CC -----  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: D21072; BAA04648.1; -  
 DR EMBL: L12029; AAA40100.1; -  
 DR EMBL: L12030; AAA40101.1; -  
 DR EMBL: S74318; AAB32650.1; -  
 DR EMBL: D43804; BAA07862.1; -  
 DR EMBL: D43805; BAA07863.1; -  
 DR PIR: A53497; A53497.  
 DR HSP: P48061; 1SDP.  
 DR MGD: MGI:103556; Sdfl.  
 DR InterPro: IPR001089; CXC\_chemkine\_sm11.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PF00048; IL8; 1.  
 DR SMART: SM00199; SCY; 1.  
 DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; FALSE\_NEG.  
 DR Cyclic; Chemotaxis; Growth factor; Signal; Alternative splicing.  
 FT SIGNAL 1 19  
 FT CHAIN 20 89 STROMAL CELL-DERIVED FACTOR 1.  
 FT DISULFID 30 55 POTENTIAL.  
 FT DISULFID 32 71 BY SIMILARITY.  
 FT VARSPLIC 89 89 K -> KRLLM (IN ISOFORM BETA).  
 SQ SEQUENCE 89 AA: 10032 MW: C48BAD69078E55FA CRC64;  
 Query Match 94.8%; Score 343; DB 1; Length 89;  
 Best Local Similarity 95.5%; Pred. No. 6; 7e-35;  
 Matches 64: Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 KGVSPYRCPCRFESFHVAVANVKKILNTPSCALQIVARLKNNRQVCIDPKLKWIOE 60  
 DB 22 KPVSLSYRCPCRFESHIRANVKKILNTPSCALQIVARLKNNRQVCIDPKLKWIOE 81  
 QY 61 YLEKALN 67  
 DB 82 YLEKALN 88  
 RESULT 4  
 ID IL8\_CANFA STANDARD: PRT: 101 AA.  
 AC P41324;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-8 precursor (IL-8) (CXCL8).  
 GN IL8.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94010328; PubMed=7916715;  
 RA Ishikawa J., Suzuki S., Hotta K., Hirota Y., Mizuno S., Suzuki K. ;  
 RT "Cloning of a canine gene homologous to the human  
 Interleukin-8-encoding gene.";  
 RL Gene 131:305-306(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph node;  
 RX MEDLINE=95127913; PubMed=7827282;  
 RA Matsumoto Y., Mohamed A., Onodera T., Kato H., Ohashi T.,  
 RA Gotsuka R., Tsujimoto H., Hasegawa A., Furusawa S., Yoshihara K.,  
 RA Ishikawa J., Hotta K., Suzuki K., Hirota Y. ;  
 RT "Molecular cloning and expression of canine Interleukin 8 cDNA.";  
 RL Cytokine 6:455-461(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Mongrel; TISSUE=Jugular vein;  
 RX MEDLINE=95114148; PubMed=7814650;  
 RA Kukiela G.L., Smith W.C., Larosa G.J., Manning A.M.,  
 RA Mendoza L.H., Daly T.J., Hughes B.J., Youker K.A., Hawkins H.K.,  
 RA Michael L.H., Rot A., Entman M.L. ;  
 RT "Interleukin-8 gene induction in the myocardium after ischemia and  
 reperfusion in vivo.";  
 RL J. Clin. Invest. 95:89-103(1995).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Beagle;  
 RX MEDLINE=97230298; PubMed=9119462;  
 RA Straubinger R.K., Straubinger A.F., Harter L., Jacobson R.H.,  
 RA Borrelli burgdorferi migrates into joint capsules and causes an up-  
 RT regulation of interleukin-8 in synovial membranes of dogs  
 experimentally infected with ticks.";  
 RL Infect. Immun. 65:1273-1285(1997).  
 CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,  
 BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN  
 NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN  
 RESPONSE TO AN INFLAMMATORY STIMULUS.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE  
 C-X-C) (CHEMOKINE CXC).  
 CC -----  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: D28772; BAA05961.1; -  
 DR EMBL: D14285; BAA03246.1; -  
 DR EMBL: U10308; AAC48434.1; -  
 DR EMBL: AF048717; AAC05134.1; -  
 DR HSP: P10145; 1IKM.  
 DR InterPro: IPR001089; CXC\_chemkine\_sm11.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTKCXC.  
 DR SMART: SM00199; SCY; 1.  
 DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; 1.  
 DR Cyclic; Chemotaxis; Inflammatory response; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 101 INTERLEUKIN-8.  
 FT DISULFID 34 61 BY SIMILARITY.  
 FT DISULFID 36 77 BY SIMILARITY.  
 SQ SEQUENCE 101 AA: 11280 MW: 3A3A4676DA968376 CRC64;  
 Query Match 28.2%; Score 102; DB 1; Length 101;

Best Local Similarity 36.1%; Pred. No. 1.3e-05;  
Matches 26; Conservative 15; Mismatches 19; Indels 12; Gaps 5;

OY 3 VSPSYRCPCHFFESHVAVAN---VKHLKIINT--PNCALQIYARKNNNOVCIDPKLKW 57  
DB 28 VSSSELKQC--IKHTSPFKIKELVIDSGPHCENSEIIVKLVN-ECVCLDPKRW 84

OY 58 IOE---YLEKA 65  
DB 85 VOKVVOIFLKA 96

RESULT 5

ID IL8\_CAVPO STANDARD; PRT; 101 AA.

AC P4913;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Interleukin-8 precursor (IL-8) (CXCL8) (Neutrophil attractant protein 1) (NAP-1).

GN IL8.

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.

NCBI\_TaxID=10141;

OX [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RX MEDLINE=94065176; PubMed=7504015;

RA Yoshimura T., Johnson D.G.;

RT "CDNA cloning and expression of guinea pig neutrophil attractant protein-1 (NAP-1). NAP-1 is highly conserved in guinea pig.";

RL J Immunol 151:6225-6236(1993)

CC -!- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS, BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).

CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXCL).

CC -----

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CC -----

CC EMBL: L04986; AAA37049.1; -

DR HSSP: P10145; 2118

DR InterPro: IPR001089; CXC\_chmkine\_sm11.

DR InterPro: IPR001811; Chemokine\_IL8.

DR Pfam: PF00048; IL8; 1.

DR PRINTS: PR00437; SMALLCYTKCXC.

DR SMART: SM00199; SCY; 1.

DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; 1.

KW Cytokine; Chemotaxis; Inflammatory response; Signal.

FT SIGNAL 1 22 BY SIMILARITY.

FT CHAIN 23 101 INTERLEUKIN-8.

FT DISULFID 34 61 BY SIMILARITY.

FT DISULFID 36 77 BY SIMILARITY.

SO SEQUENCE 101 AA; 11414 MW; 557E2A9E15F6727F CRC64;

Query Match

Best Local Similarity 27.9%; Score 101; DB 1; Length 101;

Matches 23; Conservative 16; Mismatches 17; Indels 8; Gaps 5;

OY 8 RCRCRPFESHVAVAN---VKHLKIINT--PNCALQIYARKNNNOVCIDPKLKW 62  
DB 33 RCQC--IKHTSPFKIKELVIDSGPHCENSEIIVKLVN-ECVCLDPKRW 89

OY 63 EKAL 66  
DB 90 SMFL 93

RESULT 6

ID IL8\_FELCA STANDARD; PRT; 101 AA.

AC Q9XSX5;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Interleukin-8 precursor (IL-8) (CXCL8).

GN IL8.

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedata; Felidae; Felis.

NCBI\_TaxID=9685;

OX [1]

RP SEQUENCE FROM N.A.

RA Straubinger A.F., Simpson K.W., Straubinger R.K.;

RT "Feline interleukin-8 mRNA";

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS, BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).

CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXCL).

CC -----

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CC -----

CC EMBL: AF158598; AAD40323.1; -

DR HSSP: P10145; 11KM

DR InterPro: IPR001089; CXC\_chmkine\_sm11.

DR InterPro: IPR001811; Chemokine\_IL8.

DR Pfam: PF00048; IL8; 1.

DR PRINTS: PR00437; SMALLCYTKCXC.

DR SMART: SM00199; SCY; 1.

DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; 1.

KW Cytokine; Chemotaxis; Inflammatory response; Signal.

FT SIGNAL 1 22 BY SIMILARITY.

FT CHAIN 23 101 INTERLEUKIN-8.

FT DISULFID 34 61 BY SIMILARITY.

FT DISULFID 36 77 BY SIMILARITY.

SO SEQUENCE 101 AA; 11165 MW; 690D97F13EF79170 CRC64;

Query Match

Best Local Similarity 27.3%; Score 99; DB 1; Length 101;

Matches 22; Conservative 18; Mismatches 18; Indels 8; Gaps 5;

OY 3 VSPSYRCPCHFFESHVAVAN---VKHLKIINT--PNCALQIYARKNNNOVCIDPKLKW 57  
DB 28 VSSSELKQC--IKHTSPFKIKELVIDSGPHCENSEIIVKLVN-ECVCLDPKRW 84

OY 58 IOEYLE 63  
DB 85 VOKVVE 90

RESULT 7

ID IL8\_HUMAN STANDARD; PRT; 99 AA.

AC P10145; Q9C077; Q9RG6;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-8 precursor (IL-8) (CXCL8) (Monocyte-derived neutrophil  
 DE chemotactic factor) (MDNCF) (T-cell chemotactic factor) (Neutrophil-  
 DE activating protein 1) (NAP-1) (Lymphocyte-derived neutrophil-  
 DE activating factor) (LYNAF) (Protein 3-10C) (Neutrophil-activating  
 DE factor) (NAF) (Granulocyte chemotactic protein 1) (GCP-1) (Emotactin).  
 GN IL8.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxId:9606;  
 RN 11)  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=88258376; PubMed=3260265;  
 RA Matsushima K., Morishita K., Yoshimura T., Iavii S., Kobayashi Y.,  
 RA Lew M., Appella E., Kung H., Leonard E.J., Oppenheim J.J.;  
 RT "Molecular cloning of a human monocyte-derived neutrophil chemotactic  
 RT factor (MDNCF) and the induction of MDNCF mRNA by interleukin 1 and  
 RT tumor necrosis factor.";  
 RL J. Exp. Med. 167:1883-1893(1988).  
 RN 12)  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=87224164; PubMed=2953813;  
 RA Schmid J., Weissmann C.;  
 RT "Induction of mRNA for a serine protease and a  
 RT beta-thromboglobulin-like protein in mitogen-stimulated human  
 RT leukocytes.";  
 RL J. Immunol. 139:250-256(1987).  
 RN 13)  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=89313739; PubMed=2664463;  
 RA Kowalski J., Denhardt D.T.;  
 RT "Regulation of the mRNA for monocyte-derived neutrophil-activating  
 RT peptide in differentiating HL60 promyelocytes.";  
 RL Mol. Cell. Biol. 9:1946-1957(1989).  
 RN 14)  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=89309826; PubMed=2663993;  
 RA Mukaida N., Shitroo M., Matsushima K.;  
 RT "Genomic structure of the human monocyte-derived neutrophil  
 RT chemotactic factor IL-8.";  
 RL J. Immunol. 143:1366-1371(1989).  
 RN 15)  
 RN SEQUENCE FROM N.A.  
 RA Ishikawa J.;  
 RT Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.  
 RN 16)  
 RN SEQUENCE FROM N.A. (ISOFORM 2).  
 RA Jang J.S., Kim B.E.;  
 RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 RN 17)  
 RN SEQUENCE FROM N.A.  
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
 RA Nickerson D.A.;  
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RN 18)  
 RN SEQUENCE OF 23-46.  
 RX MEDLINE=89246368; PubMed=2655583;  
 RA Golds E.E., Mason P., Nyirkos P.;  
 RT "Inflammatory cytokines induce synthesis and secretion of gro protein  
 RT and a neutrophil chemotactic factor but not beta 2-microglobulin in  
 RT human synovial cells and fibroblasts.";  
 RL Biochem. J. 259:585-588(1989).  
 RN 19)  
 RN SEQUENCE OF 23-54.  
 RX MEDLINE=89279141; PubMed=2659722;  
 RA Suzuki K., Miyasaka H., Ota H., Yamakawa Y., Tagawa M., Kuramoto A.,  
 RA Mizuno S.;  
 RT "Purification and partial primary sequence of a chemotactic protein  
 RT for polymorphonuclear leukocytes derived from human lung giant cell  
 RT carcinoma LU65C cells.";  
 RL J. Exp. Med. 169:1895-1901(1989).  
 RN 10)  
 RN SEQUENCE OF 28-99.  
 RX MEDLINE=88162914; PubMed=3279957;  
 RA Gregory H., Young J., Schroeder J.M., Mrowietz U., Christophers E.;  
 RT "Structure determination of a human lymphocyte derived neutrophil  
 RT activating peptide (LYNAF).";  
 RL Biochem. Biophys. Res. Commun. 151:883-890(1988).  
 RN 111)  
 RN SEQUENCE OF 28-59.  
 RX MEDLINE=88106502; PubMed=3322281;  
 RA Walz A., Feverl P., Aschauer H., Baggiolini M.;  
 RT "Purification and amino acid sequencing of NAF, a novel neutrophil-  
 RT activating factor produced by monocytes.";  
 RL Biochem. Biophys. Res. Commun. 149:755-761(1987).  
 RN 112)  
 RN SEQUENCE OF 28-69.  
 RX MEDLINE=88097462; PubMed=3480540;  
 RA Yoshimura T., Matsushima K., Tanaka S., Robinson E.A., Appella E.,  
 RA Oppenheim J.J., Leonard E.J.;  
 RT "Purification of a human monocyte-derived neutrophil chemotactic  
 RT factor that has peptide sequence similarity to other host defense  
 RT cytokines.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:9233-9237(1987).  
 RN 113)  
 RN N-TERMINAL FORMS.  
 RX MEDLINE=91006326; PubMed=2145175;  
 RA van Damme J., Rampart M., Coning R., Decock B., van Osselaer N.,  
 RA Willems J., Billiau A.;  
 RT "The neutrophil-activating proteins interleukin 8 and beta-  
 RT thromboglobulin: in vitro and in vivo comparison of NH2-terminally  
 RT processed forms.";  
 RL Eur. J. Immunol. 20:2113-2118(1990).  
 RN 114)  
 RN N-TERMINAL FORMS.  
 RX MEDLINE=89231715; PubMed=2523801;  
 RA van Damme J., van Beeumen J., Conings R., Decock B., Billiau A.;  
 RT "Purification of granulocyte chemotactic peptide/interleukin-8  
 RT reveals N-terminal sequence heterogeneity similar to that of  
 RT beta-thromboglobulin.";  
 RL Eur. J. Biochem. 181:337-344(1989).  
 RN 115)  
 RN SYNTHESIS OF 28-99.  
 RX MEDLINE=91175767; PubMed=2007144;  
 RA Clark-Lewis I., Mose B., Walz A., Baggiolini M., Scott G.J.,  
 RA Aebbersold R.;  
 RT "Chemical synthesis, purification, and characterization of two  
 RT inflammatory proteins, neutrophil activating peptide 1  
 RT (interleukin-8) and neutrophil activating peptide.";  
 RL Biochemistry 30:3128-3135(1991).  
 RN 116)  
 RN REVIEW.  
 RX MEDLINE=92347562; PubMed=1639201;  
 RA Baggiolini M., Clark-Lewis I.;  
 RT "Interleukin-8, a chemotactic and inflammatory cytokine.";  
 RL FEBS Lett. 307:97-101(1992).  
 RN 117)  
 RN STRUCTURE BY NMR.  
 RX MEDLINE=90234679; PubMed=2184886;  
 RA Clore G.M., Appella E., Yamada M., Matsushima K., Gronenborn A.M.;  
 RT "Three-dimensional structure of interleukin 8 in solution.";  
 RL Biochemistry 29:1689-1696(1990).  
 RN 118)  
 RN STRUCTURE BY NMR OF COMPLEX TO RECEPTOR.  
 RX MEDLINE=99148123; PubMed=10368283;  
 RA Skelton N.J., Quan C., Reilly D., Loman H.;  
 RT "Structure of a CXCL chemokine-receptor fragment in complex with  
 RT interleukin-8.";  
 RL Structure 7:157-168(1999).  
 RN 119)  
 RN X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 RX MEDLINE=90216714; PubMed=2182630;  
 RA Baldwin E.T., Franklin K.A., Appella E., Yamada M., Matsushima K.,  
 RA Wlodawer A., Weber I.T.;  
 RT "Crystallization of human interleukin-8. A protein chemotactic for

```

RT  neutrophils and T-lymphocytes."
RL  J. Biol. Chem. 265:6851-6853(1990).
[20]
RX  X-RAY CRYSTALLOGRAPHY, AND STRUCTURE BY NMR.
RA  MEDLINE=91171286; PubMed=2005614;
RA  Clore G.M., Gronenborn A.M.;
RT  "Comparison of the solution nuclear magnetic resonance and crystal
RT  structures of interleukin-8. Possible implications for the mechanism
RT  of receptor binding."
RL  J. Mol. Biol. 217:611-620(1991).
[21]
RX  X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS), AND STRUCTURE BY NMR.
RA  MEDLINE=91110556; PubMed=1988949;
RA  Baldwin E.T., Weber I.T., St Charles R., Xuan J.C., Appella E.,
RA  Baldwin M., Matsushima K., Edwards B.F., Clore G.M., Gronenborn A.M.;
RT  "Crystal structure of interleukin 8: symbiosis of NMR and
RT  crystallography."
RL  Proc. Natl. Acad. Sci. U.S.A. 88:502-506(1991).
[22]
RX  X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF MUTANT.
RA  Garber N., Lomnan H., Artis D.R., Eigenbrodt C.;
RT  "Receptor-binding conformation of the 'ELR' motif of IL-8: X-ray
RT  structure of the LSC/H3C variant at 2.35 A resolution."
RL  Proteins 38:361-367(2000).
CC  -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC  BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC  NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC  RESPONSE TO AN INFLAMMATORY STIMULUS.
CC  -1- SUBUNIT: HOMODIMER.
CC  -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC  C-X-C) (CHEMOKINE CXCL).
-----
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DR  EMBL: Y00787; CA68742.1; -
DR  EMBL: M17017; AAA35611.1; -
DR  EMBL: M26383; AAA36323.1; -
DR  EMBL: M28130; AAA59158.1; -
DR  EMBL: D14283; BAA03245.1; -
DR  EMBL: AF043337; AAK00048.1; -
DR  EMBL: AF385628; AAK60276.1; ALT_SEQ.
DR  PIR: A37034; A37034.
DR  PIR: S03975; S03975.

Query Match      26.0%; Score 94; DB 1; Length 99;
Best Local Similarity 32.3%; Pred. No. 0.00012;
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

QY  8 RCPG-REFRESHARANKHLKILNT-PNCA-IQIVARLKNNNROVCIDPKLWIOEYLEK 64
    11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db  33 RCGIKTYKRFHFKFIKELRVIESGPHCANTEIIVKL-SGRELCDPRENNVQVAVEK 91
    65 AL 66
QY  1
Db  92 FL 93

RESULT 8
ID  IL8_SHEEP STANDARD; PRT; 101 AA.
AC  P36925;
DT  01-JUN-1994 (Rel. 29, Created)
DT  01-JUN-1994 (Rel. 29, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Interleukin-8 precursor (IL-8) (CXCL8).
GN  IL8.

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OS  Ovis aries (Sheep).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovidae; Caprinae; Ovis.
OX  NCBI_TaxID=9940;
RN  [1]
RX  SEQUENCE FROM N.A.
RA  MEDLINE=95121931; PubMed=7821808;
RA  Legestelois I., Greenland T., Arnaud P., Mornex J.F., Cordier G.;
RT  "Sequencing of the ovine interleukin-8-encoding cDNA using the
RT  polymerase chain reaction."
RL  Gene 150:367-369(1994).
[2]
RX  SEQUENCE FROM N.A.
RA  MEDLINE=95137691; PubMed=7835984;
RA  Seow H.F., Yoshimura T., Wood P.R., Golditz I.G.;
RT  "Cloning, sequencing, expression and inflammatory activity in skin of
RT  ovine interleukin-8."
RL  Immunol. Cell Biol. 72:398-405(1994).
CC  -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC  BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC  NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC  RESPONSE TO AN INFLAMMATORY STIMULUS.
CC  -1- SUBUNIT: HOMODIMER.
CC  -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC  C-X-C) (CHEMOKINE CXCL).
-----
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-----
DR  EMBL: X78306; CA55115.1; -
DR  EMBL: S74436; AAB33241.1; -
DR  PIR: S42496; S42496.
DR  HSSP: P10145; 1IKM.
DR  InterPro: IPR001089; CXCL; chemokine_sm1.
DR  InterPro: IPR001811; Chemokine_IL8.
DR  Pfam: PF000048; IL8; 1.
DR  PRINTS: PR00437; SMALLCYTCKXC.
DR  SMART: SM00199; SCY; 1.
DR  PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
KW  Cytokine; Chemotaxis; Inflammatory response; Signal.
FT  STGMAL 1 22 BY SIMILARITY.
FT  CHAIN 23 101 INTERLEUKIN-8.
FT  DISULFID 34 61 BY SIMILARITY.
FT  FT 36 77 BY SIMILARITY.
SQ  SEQUENCE 101 AA; 11292 MW; 40E8418B57C56A5B CRC64;

Query Match      25.7%; Score 93; DB 1; Length 101;
Best Local Similarity 30.4%; Pred. No. 0.00016;
Matches 21; Conservative 20; Mismatches 20; Indels 8; Gaps 5;

QY  3 VSPSYRCPGFFSFHVARAN---VKHLKILNT-PNCA-IQIVARLKNNNROVCIDPKLW 57
    11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db  28 MSTELKRCQ--IKTHSPFHPKFIKELRVIESGPHCNSBIIVKL-TNGKVCOLDPKRW 84
    58 IOEYLEKAL 66
QY  1
Db  85 VQKVVQAF 93

RESULT 9
ID  GRO_MOUSE STANDARD; PRT; 96 AA.
AC  P12850;
DT  01-OCT-1989 (Rel. 12, Created)
DT  01-OCT-1989 (Rel. 12, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Growth regulated protein precursor (CXCL1) (platelet-derived growth
GN  Growth regulated protein precursor (CXCL1) (platelet-derived growth

```

DE SCFBI OR GRO1 OR GRO OR MCSA.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RN  
RX SEQUENCE FROM N.A.  
RX MEDLINE=89139485; PubMed=2917992;  
RA Oquendo P., Alberta J., Wen D., Graycar J.L., Derynck R., Stiles C.D.;  
RT "The platelet-derived growth factor-inducible KC gene encodes a  
RT secretory protein related to platelet alpha-granule proteins."  
RL J. Biol. Chem. 264:4133-4137(1989).  
RN [2]  
RN  
RP SEQUENCE FROM N.A.  
RP MEDLINE=89078502; PubMed=2909392;  
RA Ryseck R.P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;  
RT "Cloning and sequence of a secretory protein induced by growth  
RT factors in mouse fibroblasts."  
RL Exp. Cell Res. 180:266-275(1989).  
RN [3]  
RN  
RP SEQUENCE FROM N.A.  
RP STRAIN=129/SV;  
RA Bozic C.R., Kolakowski L.F. Jr., von Uexkull C., Garcia-Rodriguez M.,  
RA Conklin M.J., Breslow R., Snowell H.J., Gerard N.P., Gerard C.;  
RL Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.  
RN [4]  
RN  
RP SEQUENCE OF 1-10 FROM N.A.  
RP TISSUE=Liver;  
RC MEDLINE=96016008; PubMed=7561058;  
RA Ohmori Y., Fukunoto S., Hamilton T.A.;  
RT "Two structurally distinct kappa B sequence motifs cooperatively  
RT control LPS-induced KC gene transcription in mouse macrophages.";  
RL J. Immunol. 155:3593-3600(1995).  
CC -1- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. CONTRIBUTES TO  
CC NEUTROPHIL ACTIVATION DURING INFLAMMATION (BY SIMILARITY).  
CC -1- INDUCTION: BY PLATELET-DERIVED GROWTH FACTOR. IN LUNG, BY  
CC LIPOPOLYSACCHARIDE OR INFLAMMATION (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE  
CC C-X-C) (CHEMOKINE CXCL).  
CC -----  
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CC -----  
DR EMBL; J04596; AAA031.1; -.  
DR EMBL; J02634; AAB03376.1; -.  
DR EMBL; J02527; AAB03376.1; JOINED.  
DR EMBL; S79767; -. NOT\_ANNOTATED\_CDS.  
DR PTR; A32954; A32954.  
DR PTR; JH0081; JH0081.  
DR HSSP; P19875; IONK.  
DR MGD; MG1:108068; Gro1.  
DR InterPro: IPR001089; CXCL chemokine\_sm11.  
DR Interpro: IPR001811; Chemokine\_Il8.  
DR Pfam: PF00048; IL8; 1.  
DR PRINTS; PR00437; SMALLCYTCXC.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00471; SMALL\_CYTOKINES\_CXC; 1.  
KW Cyclokinin; Growth factor; Inflammatory response; Signal.  
FT SIGNAL 1 24 PROBABLE.  
FT CHAIN 25 96 GROWTH REGULATED PROTEIN.  
FT DISULFID 33 59 BY SIMILARITY.  
FT DISULFID 35 75 BY SIMILARITY.  
SQ SEQUENCE 96 AA: 10254 MW: 4452BSE5C38BA5C2 CRC64;

	Query Match	Best Local Similarity	Matches
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	30.3%	Pred. NO. 0.00017;	
	19;	Mismatches	3;
	24;	Indels	Gaps
			3;

QY	3	VSPSPRCRCFFESHVANANKHLKIL-L-NTPCA-LQIVARKNNRPOVCDIPKUKTIOE	60
Db	27	IANELRCOCLDTMAGIHKNIOQLKVLPSGFCHTOTEVATILK-NGREACIDPEAPLYOK	85
QY	61	YLERAL 66	
Db	86	IVOKML 91	
RESULT 10			
IL8_PIG	IL8_PIG	STANDARD:	PRF: 103 AA.
AC	P26894; P22951;		
DT	01-AUG-1991 (Rel. 19, Created)		
DT	01-AUG-1992 (Rel. 23, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Interleukin-8 precursor (IL-8) (CXCL8) (Alveolar macrophage		
DE	chemotactic factor I) (AMCF-I).		
GN	IL8.		
OS	Sus scrofa (Pig).		
OC	Euarystota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
OX	NCBI_TaxID:9823;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-94103307; Pubmed-8276881.		
RA	Lin G., Pearson A.E., Scamurra R.W., Zhou Y., Baarsch M.J.,		
RA	Weiss D.J., Murlaugh M.P.;		
RT	"Regulation of interleukin-8 expression in porcine alveolar		
RT	macrophages by bacterial lipopolysaccharide.";		
RL	J. Biol. Chem. 269:77-85(1994).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Sanjanwaia M.;		
RL	Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 26-45.		
RC	TISSUE=Lung;		
RX	MEDLINE-93041741; Pubmed-1420165.		
RA	Goodman R.B., Foster D.C., Mathewes S.L., Osborn S.G., Kuiper J.L.,		
RA	Forstrom J.W., Martin T.R.;		
RT	"Molecular cloning of porcine alveolar macrophage-derived neutrophil		
RT	chemotactic factors I and II; Identification of porcine IL-8 and		
RT	another intercrine-alpha protein.";		
RL	Biochemistry 31:10483-10490(1992).		
RN	[4]		
RP	REVISION TO 23.		
RA	Goodman R.B.;		
RL	Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.		
RN	[5]		
RP	SEQUENCE OF 26-45.		
RC	STRAIN=Yorkshire;		
RX	MEDLINE-91217086; Pubmed-1850745;		
RA	Goodman R.B., Forstrom J.W., Osborn S.G., Chi E.Y., Martin T.R.;		
RT	"Identification of two neutrophil chemotactic peptides produced by		
RT	porcine alveolar macrophages.";		
RL	J. Biol. Chem. 266:8455-8463(1991).		
CC	-I- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,		
CC	BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN		
CC	NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN		
CC	RESPONSE TO AN INFLAMMATORY STIMULUS.		
CC	-I- SUBUNIT: HOMODIMER.		
CC	-I- TISSUE SPECIFICITY: ALVEOLAR MACROPHAGES.		
CC	-I- INDUCTION: BY LIPOLYSACCHARIDE (LPS).		
CC	-I- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE		
CC	C-X-C) (CHEMOKINE CXC).		
CC	-----		
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CC	MODIFIED AND THIS STATEMENT IS NOT REMOVED. Usage by and for commercial		

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DR EMBL; M86923; AAA16616.1; -
DR EMBL; X61151; CAA43461.1; -
DR EMBL; M99367; AAG2576.1; -
DR PIR; A44253; A44253.
DR PIR; A39819; A39819.
DR HSSP; P10145; 1IKM.
DR InterPro; IPR001089; CXG_chmkline_sm1.
DR InterPro; IPR01811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTKCX.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
DR CytoKine; Chemotaxis; Inflammatory response; signal.
FT SIGNAL 1 25
FT CHAIN 26 103 INTERLEUKIN-8.
FT DISULFD 34 61 BY SIMILARITY.
FT DISULFD 36 77 BY SIMILARITY.
FT CONFLICT 33 34 RC -> CR (IN REF. 5).
FT CONFLICT 87 87 KC -> KR (IN REF. 2).
SQ SEQUENCE 103 AA; 11633 MW; 9FE0E350E1928C64 CRC64;

Query Match 25.4%; Score 92; DB 1; Length 103;
Best Local Similarity 31.8%; Pred. No. 0.00021;
Matches 21; Conservative 18; Mismatches 19; Indels 8; Gaps 5;

QY 3 VSPSYRCPCRFESHVAHAN--VHKLKIANT-PMCA-LQIYARLKNNRQCIDPKLKW 57
Db 28 VSALERKCC--INTNSTFPHRKFKELRVIESGPCENSEITIVKLV-NKEVCIDPKKKW 84
QY 58 IOEYLE 63
Db 85 YOKVVQ 90

RESULT 11
IL8_MACMU STANDARD: PRT; 101 AA.
AC P51495;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN IL8.
OS Macaca mulatta (Rhesus macaque), and
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544; 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; TISSUE=Blood;
RX MEDLINE=95355132; PubMed=7628861;
RA Minnerly J.C., Bagatoff M.P., Deppeler C.L., Keller B.T.,
RA Rapp S.R., Widomski D.L., Freland D.J., Bolanowski M.A.;
RT "Identification and characterization of rhesus macaque
RT interleukin-8";
RL Inflammation 19:313-331(1995).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
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CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERFERIN ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXCL).
-----
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-----
DR EMBL; U19849; AAA86711.1; -.
DR EMBL; U19851; AAA86713.1; -.
DR EMBL; S78555; AAA80141.2; -.
DR HSSP; P10145; 21U8.
DR InterPro; IPR001089; CXCL_chkmln-sm1.1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF000048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTKCX.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cyclokinin; Chemotaxis; Inflammatory response; Signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 101 INTERLEUKIN-8.
FT DISULFID 34 61 BY SIMILARITY.
FT DISULFID 36 77 BY SIMILARITY.
SQ SEQUENCE 101 AA; 11320 MW; 42BCEFC97C84B5F9 CRC64;

Query March 25.1%; Score 91; DB 1; Length 101;
Best local similarity 31.7%; Pred. No. 0.00028;
Matches 19; Conservative 18; Mismatches 19; Indels 4; Gaps 4;

QY 8 KCPC-RFFESHVARNVHLKILNT-PNCA-LQIVARKNNRQVCIDPKRLKIODEYLEK 64
Dy ||| : | : : | : : : | : | : | : | : | : | : | : | : | : | : | :
33 ROECKIKYTSKEPHRFKIFELRVIESGPHCANTELIVKL-SDGRELCDLPKEWVGRAVEK 91

RESULT 12
SY05_MOUSE STANDARD; PRT; 91 AA.
AC P30882;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine A5 precursor (CCLS) (T-cell specific RANTES
DE protein) (SIS-delta) (Murantes).
GN CN
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92277990; PubMed=1375672;
RX Heeger P., Wolf G., Meyers C., Sun M.J., O'Farrell S.C.,
RX Krensky A.M., Neilson E.G.;
RA "Isolation and characterization of cDNA from renal tubular epithelium
RT encoding murine Rantes."
RL Kidney Int. 41:220-225(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92289805; PubMed=1376260;
RX Schall T.J., Simpson N.J., Mak J.Y.;
RT "Molecular cloning and expression of the murine RANTES cytokine:
RT structural and functional conservation between mouse and man.";
RL Eur. J. Immunol. 22:1477-1481(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NH Swiss.
RX MEDLINE=94132613; PubMed=7507961;
RX Danoff T.M., Lalley P.A., Chang Y.S., Heeger P.S., Neilson E.G.;
RT "Cloning, genomic organization, and chromosomal localization of the
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RT SCy5 gene encoding the murine chemokine RANTES."
RL J Immunol. 152:1182-1189(1994).
RN (4)
RP SEQUENCE FROM N.A.
RC STRAIN=BAJB/C;
RX MEDLINE=94217689; PubMed=7513046;
RA Shin H.S., Drysdale B.E., Shin M.L., Noble P.W., Fisher S.N.,
  Paznekas W.A.;
RT "Definition of a lipopolysaccharide-responsive element in the 5'-
  flanking regions of Murantes and crg-2."
RL Mol. Cell. Biol. 14:2914-2925(1994).
RN (5)
RP SEQUENCE FROM N.A.
RC STRAIN=BAJB/CJ,B10.S/J, MOD/LTJ, and SJL/J; TISSUE=Spleen;
  Ma R.Z., Teuscher C.;
RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
CC -I- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
CC BASOPHILS AND ACTIVATES EOSINOPHILS.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: T-CELL AND MACROPHAGE SPECIFIC.
CC -I- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
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CC -----
DR EMBL: M77747; AAA40029.1; -
DR EMBL: S37648; AAB22330.1; -
DR EMBL: U02298; AAA18302.1; -
DR EMBL: X70675; CAA50011.1; -
DR EMBL: AF065944; AAC17511.1; -
DR EMBL: AF065945; AAC17512.1; -
DR EMBL: AF065946; AAC17513.1; -
DR EMBL: AF065947; AAC17514.1; -
DR HSSP: P13501; IRTN.
DR MGD: MGI:98262; SCy5.
DR InterPro: IPR000827; CC:Chemokine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.
FT SIGNAL 1 23
FT CHAIN 24 91
FT DISULFID 33 57
FT DISULFID 34 73
FT CONFLICT 19 19
FT CONFLICT 41 41
FT CONFLICT 41 41
SQ SEQUENCE 91 AA; 10071 MW; 5DFD66F4684FE1C8 CRC64;

Query Match 25.0%; Score 90.5; DB 1; Length 91;
Best Local Similarity 38.2%; Pred. No. 0.00028;
Matches 21; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

OY 10 PCRFESHVA--RANKHLKIINTPNCALQIYARLKNNNROYCIDPKLMIQEYL 62
DB 32 PCCFAYLSIALPRAHKEY-FYTSSKSCNMLAVFYTRNRROYCANPEKRWQVEYI 85

RESULT 13
SY05_RAT STANDARD; PRT; 92 AA.
AC P50231.
DT 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES

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DE protein) (SIS-delta).
GN SCY5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Long Evans; TISSUE=Lung;
RA Jones M.L., Shanley T.P., Ward P.A.;
RL Submitted (FEB-1994) to the EMBL/Genbank/DBJ databases.
CC -I- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
CC BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
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CC -----
DR EMBL: U06436; AAA96499.1; -
DR HSSP: P13501; IRTN.
DR InterPro: IPR000827; CC:Chemokine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.
FT SIGNAL 1 24
FT CHAIN 25 92
FT DISULFID 34 58
FT DISULFID 35 74
FT DISULFID 35 74
SQ SEQUENCE 92 AA; 10170 MW; B4FEC2B4208A9C6 CRC64;

Query Match 25.0%; Score 90.5; DB 1; Length 92;
Best Local Similarity 38.2%; Pred. No. 0.00029;
Matches 21; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

OY 10 PCRFESHVA--RANKHLKIINTPNCALQIYARLKNNNROYCIDPKLMIQEYL 62
DB 33 PCCFAYLSIALPRAHKEY-FYTSSKSCNMLAVFYTRNRROYCANPEKRWQVEYI 86

RESULT 14
IL8_BOVIN STANDARD; PRT; 101 AA.
ID IL8_BOVIN
AC P79255;
DT 01-NOV-1997 (rel. 35, Created)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN IL8.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=96304552; PubMed=8737490;
RA Morsey M.A., Popowycz Y., Kowalski J., Gerlach G., Godson D.,
  Campos M., Babiuk L.A.;
RT "Molecular cloning and expression of bovine Interleukin-8."
RL Microb. Pathog. 20:203-212(1996).
RL (2)
RP SEQUENCE FROM N.A.
RA Galligan C.L., Yoshimura T., Coomber B.L.;

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RT "Cloning and sequencing of bovine interleukin 8 cDNA isolated from  
RT lipopolysaccharide stimulated monocytes in vitro."  
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.  
CC -I- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,  
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN  
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN  
CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).  
CC -I- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -I- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE  
CC C-X-C) (CHEMOKINE CXK).  
CC -----  
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CC -----  
DR EMBL; S82598; AAB37483.1; -.  
DR EMBL; AF232704; AAF37575.1; -.  
DR HSSP; P10145; 1IKM.  
DR InterPro: IPR001089; CXK\_cmkine\_sm1.  
DR InterPro: IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR PRINTS; PR00437; SMALLCYTKCXK.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00471; SMALL\_CYTOKINES\_CXC; 1.  
DR PROSITE; PS00471; SMALL\_CYTOKINES\_CXC; 1.  
KW Cytokine; Chemotaxis; Inflammatory response; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 101  
FT DISULFID 34 61  
FT DISULFID 36 77  
FT DISULFID 36 77  
SQ SEQUENCE 101 AA: 11291 MW: 061A530507906736 CRC64:

Query Match 24.9%; Score 90; DB 1; Length 101;  
Best Local Similarity 30.3%; Pred. No. 0.00036;  
Matches 20; Conservative 20; Mismatches 18; Indels 8; Gaps 5;

OY 3 VSPSYRCPGFESHVAVRAN---VKHLKILNT-PNCA-LQIVARLKNNNROYCIDPKLKW 57  
DB 28 MSTELRCQC--IKTSTPFPKFKELRVIESGPHCENSEIIVKLTNGN-EVCLNPKRW 84  
OY 58 IOEYLE 63  
DB 85 VOKVVO 90

RESULT 15  
SZ05\_RAT  
ID SZ05\_RAT STANDARD: PRT: 130 AA.  
AC P97885:  
DT 01-NOV-1997 (rel. 35, Created)  
DT 01-NOV-1997 (rel. 35, Last sequence update)  
DT 15-JUN-2002 (rel. 41, Last annotation update)  
DE Small inducible cytokine B5 precursor (CXCL5) (Cytokine LIX).  
GN SCYB5.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RA Kellner G.S., Maciejewski-Lenoir D., Lee E.D., Maki R.A.;  
RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.  
CC -I- FUNCTION: MAY PARTICIPATE IN THE RECRUITMENT OF INFLAMMATORY CELLS  
CC BY INJURED OR INFECTED TISSUE (BY SIMILARITY).  
CC -I- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE  
CC C-X-C) (CHEMOKINE CXK).  
CC -----  
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CC -----  
DR EMBL; U90448; AAB61460.1; -.  
DR HSSP; P10889; 1M12.  
DR InterPro: IPR001089; CXK\_cmkine\_sm1.  
DR InterPro: IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR PRINTS; PR00437; SMALLCYTKCXK.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00471; SMALL\_CYTOKINES\_CXC; 1.  
KW Cytokine; Signal.  
FT SIGNAL 1 37  
FT CHAIN 38 130  
FT DISULFID 50 76  
FT DISULFID 52 93  
SQ SEQUENCE 130 AA: 14263 MW: C00F6B3605524F4E CRC64;

Query Match 24.9%; Score 90; DB 1; Length 130;  
Best Local Similarity 27.3%; Pred. No. 0.00047;  
Matches 18; Conservative 19; Mismatches 27; Indels 2; Gaps 2;

OY 3 VSPSYRCPGFESHVAVRANVKHLKILNT-PNC-ALQIVARLKNNNROYCIDPKLWIOE 60  
DB 44 VATELRGCVLTFLAPRINPMINLEVIYIPAGPHCKVEYAKLKNQNDVCLDPQAPLIRK 103  
OY 61 YLEKAL 66  
DB 104 VIOKIL 109

Search completed: January 23, 2003, 15:34:18  
Job time : 6 secs





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RESULT 2
Q90ZD1 PRELIMINARY; PRT; 89 AA.
AC Q90ZD1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Stromal cell-derived factor-1 alpha.
GN SDF-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Ohtani Y., Okada M., Kawaguchi N., Minami M., Satoh M.;
RT "cDNA cloning of rat stromal cell-derived factor-1 alpha (SDF-1
alpha).";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Pillarsetti K., Gupta S.K.;
RT "Identification and molecular cloning of a novel rat ortholog of the
alpha chemokine, stromal cell derived factor-1 (SDF-1).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF189724; AAF01066.1; -
DR EMBL: AF209976; AAG43506.1; -
DR HSP; P48061; ISDF.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 89 AA; 9977 MW; D86977626A2E35FA CRC64;

Query Match 92.8%; Score 336; DB 11; Length 89;
Best Local Similarity 94.0%; Pred. No. 1,8e-34;
Matches 63; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSFRCPCRFESHVARANKHLKILNTPNCALQIYARLNKNNROYCIDPKLWIOE 60
DB 22 KPSVLSYRCPCRFESHVARANKHLKILNTPNCALQIYARLNKNNROYCIDPKLWIOE 81
QY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 3
Q80UJ9 PRELIMINARY; PRT; 94 AA.
AC Q80UJ9;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Stromal-derived factor 1 precursor.
GN SDF-1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Braun M., Wunderlin M., Knoechel W., Gierschik P., Moepf B.;
RT "Xenopus laevis stromal-derived factor 1: conservation of structure
and function during vertebrate development.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ278857; CAC82196.1; -
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
KW Signal.

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FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 94 STROMAL-DERIVED FACTOR 1.
SQ SEQUENCE 94 AA; 10701 MW; 8C8325D152F326E7 CRC64;

Query Match 76.8%; Score 278; DB 13; Length 94;
Best Local Similarity 73.1%; Pred. No. 3.3e-27;
Matches 49; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 KGVSFRCPCRFESHVARANKHLKILNTPNCALQIYARLNKNNROYCIDPKLWIOE 60
DB 22 KPSVLSYRCPCRFESHVARANKHLKILNTPNCALQIYARLNKNNROYCIDPKLWIOE 81
QY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 4
Q91ZL1 PRELIMINARY; PRT; 91 AA.
AC Q91ZL1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE RANTES chemokine.
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RA Blanco J.C., Pletneva L.M., Prince G.A.;
RT "Sigmodon hispidus cytokines, chemokines and interferons.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF421391; AAL16932.1; -
DR InterPro: IPR000827; CC_chemkine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; UNKNOWN; 1.
SQ SEQUENCE 91 AA; 10082 MW; D0D6EABEBE4242FF CRC64;

Query Match 25.8%; Score 93.5; DB 11; Length 91;
Best Local Similarity 38.2%; Pred. No. 0.00038;
Matches 21; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 10 PCRF--FESHVARANKHLKILNTPNCALQIYARLNKNNROYCIDPKLWIOEYL 62
DB 32 PCCFAYLSAVLPRAHVKEY-FYTSKSCSNFAYVEYTRNRQVCANPKRWQDEYI 85

RESULT 5
Q80GV8 PRELIMINARY; PRT; 98 AA.
AC Q80GV8;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CXC chemokine.
GN CXC CHEMOKINE.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectidae; Paralicthyidae; Paralicthys.
NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Aoki T., Hiroo I., Lee J., Iwahori A.;
RT "Molecular cloning and expression of IL-1b and two types of chemokines
in Japanese flounder, Paralicthys olivaceus.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB070837; BAB86884.1; -

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SO SEQUENCE 98 AA: 10846 MW: 495CA839A5DBC92 CRC64:
Query Match 23.5%: Score 85; DB 13; Length 98;
Best Local Similarity 27.1%: Pred. No. 0.0048;
Matches 19; Conservative 19; Mismatches 28; Indels 4; Gaps 3;

OY 1 KGVSPSYRCPCRFESHARANVKKILKLTLPN--C-AQIYARLKNNRQVCIDPKLKW 57
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 27 RSLVSLHLCRCIETESRPIGRYIKSVETI-SPNSHCXDKTEIATLKDGVEICLDPPEAPW 85
OY 58 IOEYLEKALN 67
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 86 VKRVIINKLIS 95

RESULT 6
O90Y59 PRELIMINARY; PRT: 109 AA.
AC O90Y59
DT 01-DEC-2001 (TRMBLrel. 19, Created)
DT 01-DEC-2001 (TRMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TRMBLrel. 20, Last annotation update)
DE Interleukine-8.
GN IL-8.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralicthyidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21435923; PubMed=11551708;
RA Lee E.Y., Park H.H., Kim Y.T., Chung J.K., Choi T.J.;
RT "Cloning and sequence analysis of the interleukin-8 gene from flounder
RL (Paralicthys olivaceus).";
DR EMBL; AF216646; AAL05442.1; -.
DR Interpro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
SQ SEQUENCE 109 AA: 12117 MW: C7CE18986C50A6ED CRC64:

Query Match 23.5%: Score 85; DB 13; Length 109;
Best Local Similarity 27.1%: Pred. No. 0.0053;
Matches 19; Conservative 19; Mismatches 28; Indels 4; Gaps 3;

OY 1 KGVSPSYRCPCRFESHARANVKKILKLTLPN--C-AQIYARLKNNRQVCIDPKLKW 57
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 26 RSLVSLHLCRCIETESRPIGRYIKSVETI-SPNSHCXDKTEIATLKDGVEICLDPPEAPW 84
OY 58 IOEYLEKALN 67
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 85 VKRVIINKLIS 94

RESULT 7
O73912 PRELIMINARY; PRT: 104 AA.
AC O73912
DT 01-AUG-1998 (TRMBLrel. 07, Created)
DT 01-AUG-1998 (TRMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TRMBLrel. 20, Last annotation update)
DE K60 protein precursor (CXC chemokine K60).
GN K60.
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MACROPHAGE LIKE;
RA Sick C.;

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RN Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.
RP
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20170941; PubMed=10704244;
RA Sick C., Schneider K., Staeheli P., Weining K.C.;
RT "Novel chicken CXC and CC chemokines.";
RL Cytokine 12:181-186(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Hughes S.M., Bumstead N.;
RT "Mapping of a second ECR CXC chemokine to chicken chromosome four.";
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; Y14971; CAA75212.1; -.
DR EMBL; AF277660; AAF6485.1; -.
DR HSSP; P02775; 1PXY.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR001089; CXC_chemkine_smll.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTCCXC.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
DR signal.
FT SIGNAL
FT CHAIN
SO SEQUENCE 104 AA; 11199 MW; 83725AB91FE18E3D CRC64;

Query Match 22.4%; Score 81; DB 13; Length 104;
Best Local Similarity 29.2%; Pred. NO. 0.016;
Matches 19; Conservative 18; Mismatches 20; Indels 8; Gaps

OY 8 RCPCHFFSHAVARANKHLKILNT---PNCALQIVARLKNKNROYCIDPKLKIQEV 62
Db 33 RCQC--IEHSHKFIHPKFIQNVNLPSPGHCKNVEVIATLK-DGREVCIDPTAPWVKLI 89
OY 63 EKALN 67
Db 90 KALID 94

RESULT 8
O9YVA9 PRELIMINARY; PRT: 134 AA.
ID O9YVA9
AC O9YVA9;
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE VIL8 (CXC chemokine VIL8).
GN MDV003 OR MDV078.
OS Gallid herpesvirus 1,
OS Marek's disease herpesvirus (strain GA) (MDHV), and
OS Marek's disease herpesvirus (strain Md5) (MDHV), Turkey herpesvirus.
OS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Infectious latynotrichetis-like viruses.
CC NCBI_taxid=10386; 10388; 10389;
XX [1]
RN RN
RP SEQUENCE FROM N.A.
RP SPECIES=gallid herpesvirus 1; STRAIN=RB18;
RA Rasschaert D., Pragnet L.;
RT "Characterisation of the BamHI L fragment of the Marek's disease virus
RB18 strain (serotype 1).";
RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RP SPECIES=Marek's disease herpesvirus (strain GA) (MDHV);
RA Lin S.-F., Robinson D., Chen H.-C., Kung H.-J.;
RT "CXC chemokine encoded by Marek's Disease Virus (MDV).";
RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RP SPECIES=Marek's disease herpesvirus (strain Md5) (MDV);
RX MEDLINE=20392152; PubMed=10933706;
RA Tulman E.R., Alfonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
RT "The genome of a very virulent Marek's disease virus.";
```

RL J. Virol. 74:7980-7988(2000).  
 RN [4]  
 RP SOURCE FROM N.A.  
 RC SEQUENCES-Marek's disease herpesvirus (strain M65) (MDV);  
 RA Tullman E.R., Alfonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF314199; AAL58097.1; -  
 DR EMBL: AF065430; AAC77449.1; -  
 DR EMBL: AF243438; AAC14290.1; -  
 DR EMBL: AF243438; AAC14256.1; -  
 DR HSP: P10889; IM12.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR InterPro: IPR001089; CXCL12; Chemokine\_sm1.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTKXC.  
 DR SMART: SM00199; SCY; 1.  
 SQ SEQUENCE 134 AA; 1482 MW; C859CDB868D25190 CRC64;  
 Query Match 22.4%; Score 81; DB 12; Length 134;  
 Best Local Similarity 25.7%; Pred. No. 0.021;  
 Matches 19; Conservative 13; Mismatches 10; Indels 32; Gaps 4;  
 QY 8 RCPREFESHVARANVHKLILNTP-----NC-ALQIVARLKNRRQVC 50  
 DB 33 RCKC-----VKVTNRPGLPIAVDVIIPGICHRRTIIFALK-KNRKVC 77  
 QY 51 IDPKLKWIOEYLEK 64  
 DB 78 VDPEAPWVQOFIKK 91  
 RESULT 9  
 Q9IBJ7 PRELIMINARY; PRT; 142 AA.  
 AC Q9IBJ7;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE VIL-8.  
 GN R-LORE2.  
 OS Turkey herpesvirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Marek's disease-like viruses.  
 OC NCBI\_TaxID=10389;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-GA;  
 RX MEDLINE-92237304; PubMed-1315048;  
 RA Jones D., Lee L., Liu J.L., Kung H.J., Tilloston J.K.;  
 RT "Marek disease virus encodes a basic-leucine zipper gene resembling  
 RT the fos/ Jun oncogenes that is highly expressed in lymphoblastoid  
 RT tumors".  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4042-4046(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-GA;  
 RA Lee L.F., Wu P., Sul D., Ren D., Kung H.J.;  
 RT "The Complete UL Sequence of Serotype I Marek's Disease Virus";  
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2000).  
 DR EMBL: AF147806; AAF67205.1; -  
 DR EMBL: AF147806; AAF6793.1; -  
 DR HSP: P10889; IM12.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR InterPro: IPR001089; CXCL12; Chemokine\_sm1.  
 DR InterPro: IPR001230; Prey1\_site.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTKXC.  
 DR SMART: SM00199; SCY; 1.  
 SQ POSITIVE: PS00294; PRENYLATION; UNKNOWN.1.  
 SQ SEQUENCE 142 AA; 15770 MW; 35ABCEB9B29FDD209 CRC64;  
 Query Match 22.4%; Score 81; DB 12; Length 142;  
 Best Local Similarity 25.7%; Pred. No. 0.022;

Matches 19; Conservative 13; Mismatches 10; Indels 32; Gaps 4;  
 QY 8 RCPREFESHVARANVHKLILNTP-----NC-ALQIVARLKNRRQVC 50  
 DB 33 RCKC-----VKVTNRPGLPIAVDVIIPGICHRRTIIFALK-KNRKVC 77  
 QY 51 IDPKLKWIOEYLEK 64  
 DB 78 VDPEAPWVQOFIKK 91  
 RESULT 10  
 Q67634 PRELIMINARY; PRT; 203 AA.  
 AC Q67634;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Eco Q protein (Fragment).  
 OS Marek's disease herpesvirus (strain GA) (MDV).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Marek's disease-like viruses.  
 OC NCBI\_TaxID=10388;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-GA;  
 RX MEDLINE-96074534; PubMed-7491783;  
 RA Peng O., Zeng M., Bhuyan Z.A., Ubukata E., Tanaka A., Nonoyama M.,  
 RA Shirazi Y.;  
 RT "Isolation and characterization of Marek's disease virus (MDV) cDNAs  
 RT mapping to the BamHI-12, BamHI-Q2, and BamHI-L fragments of the MDV  
 RT genome from lymphoblastoid cells transformed and persistently infected  
 RT with MDV".  
 RL Virology 213:590-599(1995).  
 DR EMBL: U34966; AAC54629.1; -  
 DR HSP: P10889; IM12.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR InterPro: IPR001089; CXCL12; Chemokine\_sm1.  
 DR InterPro: IPR004827; TF\_bzip.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTKXC.  
 DR SMART: SM00338; BRIZ; 1.  
 DR SMART: SM00199; SCY; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 203 AA; 23132 MW; DE42F2A1C1A71C88 CRC64;  
 Query Match 22.4%; Score 81; DB 12; Length 203;  
 Best Local Similarity 25.7%; Pred. No. 0.032;  
 Matches 19; Conservative 13; Mismatches 10; Indels 32; Gaps 4;  
 QY 8 RCPREFESHVARANVHKLILNTP-----NC-ALQIVARLKNRRQVC 50  
 DB 102 RCKC-----VKVTNRPGLPIAVDVIIPGICHRRTIIFALK-KNRKVC 146  
 QY 51 IDPKLKWIOEYLEK 64  
 DB 147 VDPEAPWVQOFIKK 160  
 RESULT 11  
 Q9QYD7 PRELIMINARY; PRT; 148 AA.  
 AC Q9QYD7;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Small inducible cytokine A2.  
 GN SCY42.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-SJL/J: TISSUE=SPLEEN;  
 RX MEDLINE=96370037: PubMed=10438970;  
 RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,  
 RT Blankenhorn E.P.;  
 "Sequence polymorphisms in the chemokines Sclay (TCA-3), Sclay2  
 (monocyte chemoattractant protein (MCP)-1), and Sclay2 (MCP-5) are  
 candidates for eae7, a locus controlling susceptibility to monophasic  
 remitting/nonrelapsing experimental allergic encephalomyelitis.";  
 RL J. Immunol. 163:2262-2266(1999).  
 DR EMBL: AF065929; AAF15379.1; -;  
 DR HSSP: MGI:38259; SCY2.  
 DR HSSP: P13500; 1DOK.  
 DR InterPro: IPR000827; CC\_Chemokine\_sml.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PF00048; IL8; 1.  
 DR SMART: SM00472; SCY; 1.  
 DR PROSITE: PS00479; SMALL\_CYTOKINES\_CC; 1.  
 SO SEQUENCE 148 AA; 16268 MW; 2BA24C5D19C489EB CRC64;

Query Match 22.1%; Score 80; DB 11; Length 148;  
 Best Local Similarity 24.6%; Pred. No. 0.031;

Matches 15; Conservative 14; Mismatches 32; Indels 0; Gaps 0;

OY 3 VSPSYRCPREFSHVARANVHKILITNPNCALQIVARLKNRRNOVCIDPKLWIOEYL 62  
 ID 093442 PRELIMINARY; PRT; 101 AA.  
 AC 093442;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE LFCA-1 protein precursor.  
 OS Lampetra fluviatilis (Silver lamprey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hypoecartia;  
 OC Petromyzontiformes; Petromyzontidae; Lampetra.  
 OX NCBI\_Taxid=7748;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LEUCOCYTES;  
 RA Najakshin A.M., Mechetina L.V., Alabyev B.Y., Tarantin A.V.;  
 RT "Identification of the interleukin 8 homologue in lamprey (Lampetra  
 fluviatilis): early evolutionary divergence of chemokines.";  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ231072; CAA1314.1; -;  
 DR HSSP: P02775; 1TVX.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR InterPro: IPR001089; CXCL12; 1.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTKCXC.  
 DR SMART: SM00199; SCY; 1.  
 FT SIGNAL. 1 22 POTENTIAL.  
 FT CHAIN 23 101 LFCA-1 PROTEIN.  
 SO SEQUENCE 101 AA; 11095 MW; 80CFEB1EA7336D2 CRC64;

Query Match 22.0%; Score 79.5; DB 13; Length 101;  
 Best Local Similarity 26.9%; Pred. No. 0.024;

Matches 18; Conservative 16; Mismatches 22; Indels 11; Gaps 4;

OY 8 RCPCRFESHVARANV--KHLK----ILNTPNCA-IQIVARLKNRRNOVCIDPKLWIOE 60  
 ID 093442 PRELIMINARY; PRT; 101 AA.  
 AC 093442;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE LFCA-1 protein precursor.  
 OS Lampetra fluviatilis (Silver lamprey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hypoecartia;  
 OC Petromyzontiformes; Petromyzontidae; Lampetra.  
 OX NCBI\_Taxid=7748;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LEUCOCYTES;  
 RA Najakshin A.M., Mechetina L.V., Alabyev B.Y., Tarantin A.V.;  
 RT "Identification of the interleukin 8 homologue in lamprey (Lampetra  
 fluviatilis): early evolutionary divergence of chemokines.";  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ231072; CAA1314.1; -;  
 DR HSSP: P02775; 1TVX.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR InterPro: IPR001089; CXCL12; 1.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTKCXC.  
 DR SMART: SM00199; SCY; 1.  
 FT SIGNAL. 1 22 POTENTIAL.  
 FT CHAIN 23 101 LFCA-1 PROTEIN.  
 SO SEQUENCE 101 AA; 11095 MW; 80CFEB1EA7336D2 CRC64;

DB 86 VISHLD 92

RESULT 13

ID 028724 PRELIMINARY; PRT; 108 AA.

AC 028724;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-AUG-1999 (TREMBLrel. 11, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE GRO (Permeability factor 2).

GN RPF2.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euteria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_Taxid=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NEW ZEALAND WHITE.

RA Yoshimura T., Modi W.S.;

RT "Isolation of novel GRO genes, and a phylogenetic analysis of the CXCL12

submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE OF 43-108 FROM N.A.

RC STRAIN=NEW ZEALAND WHITE.

RX MEDLINE=95129889; PubMed=7828903;

RA Johnson M.C., Goodman R.B. II, Kajikawa O., Wong V.A., Mongovin S.M.,

RT "Cloning of two rabbit GRO homologues and their expression in alveolar

macrophages.";

RL Gene 151:337-338(1994).

DR EMBL: U95808; AAB93924.1; -;

DR EMBL: L28933; AAB6975.1; -;

DR HSSP: P19875; 1ONK.

DR InterPro: IPR001811; Chemokine\_IL8.

DR InterPro: IPR001089; CXCL12; 1.

DR Pfam: PF00048; IL8; 1.

DR PRINTS: PR00437; SMALLCYTKCXC.

DR SMART: SM00199; SCY; 1.

DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; 1.

SO SEQUENCE 108 AA; 11261 MW; 9C278041FC7A5BAD CRC64;

Query Match 22.0%; Score 79.5; DB 6; Length 108;

Best Local Similarity 27.4%; Pred. No. 0.026;

Matches 17; Conservative 21; Mismatches 21; Indels 3; Gaps 3;

OY 8 RCPCRFESHVARANVHKILITNPNCALQIVARLKNRRNOVCIDPKLWIOEYLEKA 65

DB 43 RCQCLQTVGCIHLKSIQSLVSPGPHCAQTEVIATLK-SGQECINPAPPAKKFLQKR 101

OY 66 LN 67

DB 102 LS 103

RESULT 14

ID 098702 PRELIMINARY; PRT; 97 AA.

AC 098702;

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Putative interleukin 8 (Putative cxc chemokine precursor).

GN IL-8.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI\_Taxid=8022;

RN [1]

RP SEQUENCE FROM N.A.

```
Oy      3 VSPSYRCPCHFFESHVBARANYKHLKLNT-PMCA-LQIVARLKNNNRQCIDPKLWIOE 60
        | : || |       : | ::|||   |:| ::|| | : :|::| :| :|
Db     30 VANELRCQCLQTMAVGHFKNISLKVTPPGPHCTOTEVIA TLK -NGOEACLNPEAPVOK 80
Oy      61 YLEKATL 66
        ::|| |
Db      89 IVQAKML 94
```

Search completed: January 23, 2003, 15:36:19  
Job time : 22.6 secs



PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 XX Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;  
 PI Clark-Lewis I, Salari H;  
 XX WPI: 2002-106073/14.  
 DR  
 PT Promoting the rate of haematopoietic cell multiplication for treating a  
 PT cancer involves administering chemokine receptor antagonist to the  
 PT cells -  
 XX  
 PS Claim 9: Page 54; 68pp; English.  
 XX  
 CC The invention relates to a method of promoting the rate of haematopoietic  
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)  
 CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist  
 CC has cytostatic and immunosuppressive activity and is useful for treating  
 CC cancer or autoimmune disease in a patient; to promote the rate of  
 CC haematopoietic cell multiplication; to formulate a medicament for  
 CC increasing the circulation of the haematopoietic cells in a patient; for  
 CC mobilising haematopoietic cells from a narrow locus to a peripheral blood  
 CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The  
 CC CXCR4 antagonists stimulates haematopoietic cell multiplication,  
 CC self-renewal, expansion and proliferation of peripheralisation in vivo.  
 CC  
 XX  
 SQ Sequence 67 AA;  
 Query Match Best Local Similarity 100.0%; Score 362; DB 23; Length 67;  
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 KGVSLPFCPCRFESHVARANYKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60  
 DB 1 KGVSLPFCPCRFESHVARANYKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60  
 OY 61 YLEKALN 67  
 DB 61 YLEKALN 67  
 DE 20-MAY-2002 (first entry)  
 XX  
 DE CXCR4 peptide antagonist SEQ ID NO 1.  
 XX  
 KW CRCX4: haematopoietic cell; chemokine receptor-4; cytostatic;  
 KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;  
 KW cell multiplication.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200185196-A2.  
 PD 15-NOV-2001.  
 XX  
 PF 09-MAY-2001; 2001WO-CA00659.  
 XX  
 PR 09-MAY-2000; 2000CA-2305787.  
 PR 19-MAY-2000; 2000US-205467P.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 PI Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;  
 PI Clark-Lewis I, Salari H;  
 XX WPI: 2002-106073/14.  
 DR  
 XX

PT Promoting the rate of haematopoietic cell multiplication for treating a  
 PT cancer involves administering chemokine receptor antagonist to the  
 PT cells -  
 XX  
 PS Claim 9: Page 54; 68pp; English.  
 XX  
 CC The invention relates to a method of promoting the rate of haematopoietic  
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)  
 CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist  
 CC has cytostatic and immunosuppressive activity and is useful for treating  
 CC cancer or autoimmune disease in a patient; to promote the rate of  
 CC haematopoietic cell multiplication; to formulate a medicament for  
 CC increasing the circulation of the haematopoietic cells in a patient; for  
 CC mobilising haematopoietic cells from a narrow locus to a peripheral blood  
 CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The  
 CC CXCR4 antagonists stimulates haematopoietic cell multiplication,  
 CC self-renewal, expansion and proliferation of peripheralisation in vivo.  
 CC  
 XX  
 SQ Sequence 67 AA;  
 Query Match Best Local Similarity 97.8%; Score 354; DB 23; Length 67;  
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 KGVSLPFCPCRFESHVARANYKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60  
 DB 1 KGVSLPFCPCRFESHVARANYKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60  
 OY 61 YLEKALN 67  
 DB 61 YLEKALN 67  
 DE 20-MAY-2002 (first entry)  
 XX  
 DE CXCR4 peptide antagonist SEQ ID NO 2.  
 XX  
 KW CRCX4: haematopoietic cell; chemokine receptor-4; cytostatic;  
 KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;  
 KW cell multiplication.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200185196-A2.  
 PD 15-NOV-2001.  
 XX  
 PF 09-MAY-2001; 2001WO-CA00659.  
 XX  
 PR 09-MAY-2000; 2000CA-2305787.  
 PR 19-MAY-2000; 2000US-205467P.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 PI Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;  
 PI Clark-Lewis I, Salari H;  
 XX WPI: 2002-106073/14.  
 DR  
 XX

Key Location/Qualifiers  
 Modified-site 5  
 /note="Optionally the proline analogue 6-amino-7-oxo-2,3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic acid residue or a bicyclic turned dipeptide (Btd)"



PT Promoting the rate of haematopoietic cell multiplication for treating a  
PT cancer involves administering chemokine receptor antagonist to the  
PT cells -  
XX  
PS Claim 9; Page 54; 68pp; English.  
XX  
CC The invention relates to a method of promoting the rate of haematopoietic  
CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)  
CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist  
CC has cytostatic and immunosuppressive activity and is useful for treating  
CC cancer or autoimmune disease in a patient; to promote the rate of  
CC haematopoietic cell multiplication; to formulate a medicament for  
CC increasing the circulation of the haematopoietic cells in a patient; for  
CC mobilising haematopoietic cells from a narrow locus to a peripheral blood  
CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The  
CC CXCR4 antagonists stimulates haematopoietic cell multiplication,  
CC self-renewal, expansion and proliferation of peripheralisation in vivo.  
XX  
SQ Sequence 67 AA:  
  
Query Match 95.9%; Score 347; DB 23; Length 67;  
Best Local Similarity 97.0%; Pred. No. 2.6e-38;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
OY 1 KGVSLPYRCPCRPFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60  
Db 1 KGVSLPYRCPCRPFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60  
  
OY 61 YLEKALN 67  
Db 61 YLEKALN 67  
  
RESULT 4  
AAM48660  
ID AAM48660 standard; peptide: 67 AA.  
XX  
AC AAM48660;  
XX  
DT 20-MAY-2002 (first entry)  
XX  
DE CXCR4 peptide antagonist SEQ ID NO 5.  
XX  
KW CRCX4: haematopoietic cell; chemokine receptor-4; cytostatic;  
KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;  
KW cell multiplication.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 8 /note="Optionally the proline analogue 6-amino-7-oxo-2,  
FT 3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic  
FT acid residue"  
XX  
PN WO200185196-A2.  
XX  
PD 15-NOV-2001.  
XX  
PF 09-MAY-2001; 2001WO-CA00659.  
XX  
PR 09-MAY-2000; 2000CA-2305787.  
PR 19-MAY-2000; 2000US-205467P.  
XX  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
XX  
PI Tuden CR, Metzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;  
PI Clark-Lewis I, Salari H;  
XX  
DR WPI; 2002-106073/14.  
XX  
PT Promoting the rate of haematopoietic cell multiplication for treating a

PT cancer involves administering chemokine receptor antagonist to the  
PT cells -  
XX  
PS Claim 9; Page 54; 68pp; English.  
XX  
CC The invention relates to a method of promoting the rate of haematopoietic  
CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)  
CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist  
CC has cytostatic and immunosuppressive activity and is useful for treating  
CC cancer or autoimmune disease in a patient; to promote the rate of  
CC haematopoietic cell multiplication; to formulate a medicament for  
CC increasing the circulation of the haematopoietic cells in a patient; for  
CC mobilising haematopoietic cells from a narrow locus to a peripheral blood  
CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The  
CC CXCR4 antagonists stimulates haematopoietic cell multiplication,  
CC self-renewal, expansion and proliferation of peripheralisation in vivo.  
XX  
SQ Sequence 67 AA:  
  
Query Match 95.9%; Score 347; DB 23; Length 67;  
Best Local Similarity 97.0%; Pred. No. 2.6e-38;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
OY 1 KGVSLPYRCPCRPFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60  
Db 1 KGVSLPYRCPCRPFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60  
  
OY 61 YLEKALN 67  
Db 61 YLEKALN 67  
  
RESULT 5  
AAM50760  
ID AAM50760 standard; peptide: 67 AA.  
XX  
AC AAM50760;  
XX  
DT 27-JUL-1998 (first entry)  
XX  
DE Peptide which binds to CXCR4 receptor and is useful for treating HIV.  
XX  
KW Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus;  
KW HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.  
XX  
OS Homo sapiens.  
XX  
PN FR2751658-A1.  
PN 30-JAN-1998.  
PD  
XX  
PF 26-JUL-1996; 96FR-0009477.  
XX  
PR 26-JUL-1996; 96FR-0009477.  
XX  
PA (INSP ) INST PASTEUR.  
XX  
PI Arenzana SF, Baggiolini M, Clark LI, Moser B, Virelizier JL;  
PI WPI; 1998-123039/12.  
XX  
DR Human stromal cell-derived chemokine, SDF-1 - useful for treating  
PT human immunodeficiency virus infection  
XX  
PS Claim 2; Page 29; 48pp; French.  
XX  
CC The invention relates to peptides which bind to a cellular receptor for  
CC CXC chemokines, namely the CXCR4 receptor (also known as leukocyte-  
CC expressed transmembrane domain receptor), especially where the  
CC peptide is human chemokine SDF-1. The peptide can be used to treat or  
CC prevent HIV infections, optionally together with reverse transcriptase  
CC inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4  
CC receptor antagonists, immunotherapy agents, agents for treating HIV-

CC associated opportunistic infections and/or other CXC or CC chemokines,  
 CC especially RANTES, MIP-1 alpha, MIP-1 beta or MCP-1. The peptide can be  
 CC used to detect anti-SDF-1 antibodies in biological fluids. This  
 CC sequence represents a specifically claimed peptide which binds to the  
 CC CXCR4 receptor.

XX  
 SQ Sequence 67 AA;

Query Match 95.6%; Score 346; DB 19; Length 67;  
 Best Local Similarity 97.0%; Pred. No. 3.5e-38;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60  
 DB 1 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60

OY 61 YLEKALN 67  
 DB 61 YLEKALN 67

RESULT 6  
 AAY34092

ID AAY34092 standard; protein; 67 AA.

AC AAY34092;

DT 29-NOV-1999 (first entry)

DE Native stromal cell derived factor 1 (SDF-1) alpha protein.

KW CXC chemokine receptor 4; CXCR4; antagonist; medicament; T-cell;  
 KM interferon gamma; autoimmune disease; multiple sclerosis; cancer;  
 KM angiogenesis; stromal cell derived factor 1; SDF-1.

OS Mammalia.

PN W09947158-A2.

PD 23-SEP-1999.

PF 12-MAR-1999; 99WO-CA00221.

PR 13-MAR-1998; 98CA-2226391.

PR 14-AUG-1998; 98CA-2245224.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Clark-Lewis I, Gong J, Durotojo V;

DR WPI; 1999-561857/47.

PT Use of CXC chemokine receptor 4 for treating autoimmune disease and  
 cancer

XX Example 1; Fig 1; 71pp; English.

CC The invention relates to the use of a CXC chemokine receptor 4 (CXCR4)  
 CC antagonist for the manufacture of a medicament for reducing Interferon  
 CC gamma production by T-cells in a mammal. The CXCR4 antagonist can be used  
 CC to treat or to design a medicament to treat, an autoimmune disease,  
 CC multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4  
 CC antagonists may be peptide compounds comprising a substantially purified  
 CC peptide fragment, analogue or a pharmacologically acceptable salt of  
 CC stromal cell derived factor 1 (SDF-1). The present sequence represents  
 CC the amino acid sequence of SDF-1 alpha protein.

XX  
 SQ Sequence 67 AA;

Query Match 95.6%; Score 346; DB 20; Length 67;  
 Best Local Similarity 97.0%; Pred. No. 3.5e-38;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60  
 DB 1 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60

OY 61 YLEKALN 67  
 DB 61 YLEKALN 67

RESULT 7  
 AAY06741

ID AAY06741 standard; protein; 67 AA.

AC AAY06741;

DT 18-JUN-1999 (first entry)

DE SDF-1 alpha/RANTES cross-over chemokine control molecule SSSS.

KW Chemokine; cross-over protein; pharmaceutical; inflammatory; AIDS; viral;  
 KM infectious disease; hematopoiesis; chemoprotection; asthma; RANTES; VMP;  
 KM allergic rhinitis; atopic dermatitis; rheumatoid arthritis; SDF-1; MPV;  
 KM stromal cell derived factor 1; Macrophage Inflammatory protein.

OS Synthetic.

OS Homo sapiens.

PN W09911655-A1.

PD 11-MAR-1999.

PF 31-AUG-1998; 98WO-US18096.

PR 04-SEP-1997; 97US-0057620.

XX (GRYP-) GRYPHON SCI.

XX Kent SBH, Stani MA, Simon R, Wilken J;

DR WPI; 1999-205128/17.

PT New cross-over proteins for treatment of inflammation and infections  
 e.g. AIDS - prepared by ligation of two functional protein modules  
 derived from two different parent molecules

XX Example 4; Page 43; 75pp; English.

CC The invention relates to a cross-over protein produced by chemical  
 CC ligation of at least two functional protein modules derived from at  
 CC least two parent protein molecules. The cross-over proteins can be used  
 CC in pharmaceutical compositions for therapy of inflammatory and  
 CC infectious diseases including AIDS, and for indications of hematopoiesis  
 CC and chemoprotection. They are also useful for treatment of asthma,  
 CC allergic rhinitis, atopic dermatitis and rheumatoid arthritis. A library  
 CC comprising a collection of cross-over proteins is useful for screening  
 CC for cross-over proteins that are receptor ligands. The libraries  
 CC comprise functionally diverse compounds therefore improving the drug  
 CC discovery process. The proteins and libraries are exemplified by the  
 CC preparation of cross-over chemokines comprising various combinations of  
 CC peptide segments derived from RANTES, SDF-1 (stromal cell derived factor  
 CC 1), VMP (viral Macrophage Inflammatory protein) and other such  
 CC chemokines. Sequences AAY06741-62 represent amino acid sequences of SDF-1  
 CC alpha/RANTES cross-over molecules.

XX  
 SQ Sequence 67 AA;

Query Match 95.6%; Score 346; DB 20; Length 67;  
 Best Local Similarity 97.0%; Pred. No. 3.5e-38;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60  
 DB 1 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNQVCIDPKLKWIOE 60



ID AAB47680 standard; peptide: 67 AA.  
 XX AAB47680;  
 AC  
 XX  
 DT 30-JAN-2002 (first entry)  
 XX  
 DE SDF-1-alpha.  
 XX  
 KM Hematopoietic cell; multiplication; CXCR4 chemokine receptor 4; CXCR4;  
 KM agonist; stromal cell derived factor one; SDF-1; autoimmune disease;  
 KM macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;  
 KM autologous; allogenic; bone marrow; stem cell; transplantation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200176615-A2.  
 PD  
 XX 18-OCT-2001.  
 PF  
 XX 12-APR-2001; 2001MO-CA00540.  
 PR 12-APR-2000; 2000CA-2305036.  
 PR 14-SEP-2000; 2000US-232425P.  
 PR 23-FEB-2001; 2001CA-2335109.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 XX  
 PI Salati H, Merzouk A, Arab L, Tudan CR, Saxena G, Faves CJ;  
 PI Cashman J, Clark-Lewis I;  
 XX  
 DR WPI; 2002-025882/03.  
 XX  
 PT CXCR4 receptor 4 agonists that reduces hematopoietic cell multiplication  
 PT and susceptibility to cytotoxic agents, are useful for bone marrow or  
 PT peripheral blood stem cell transplantation  
 PT  
 XX  
 PS Claim 8: Page 57; 74pp: English.  
 XX  
 CC The sequences given in AAB47680-717 represent peptides which may be  
 CC used in the method of the invention for reducing the rate of  
 CC hematopoietic cell multiplication. These peptides act as CXCR4 chemokine  
 CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on  
 CC stromal cell derived factor one (SDF-1) with some also containing  
 CC sequences derived from macrophage inflammatory protein 1-alpha  
 CC (MIP-1-alpha). They can be used to reduce susceptibility of  
 CC hematopoietic cells to a cytotoxic agent, by administering one of the  
 CC agonist peptides to the cells prior to or during exposure of the  
 CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce  
 CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly  
 CC in a patient with cancer requiring autologous or allogenic bone marrow  
 CC or peripheral blood stem cell transplantation, or an autoimmune disease.  
 CC  
 XX  
 SQ Sequence 67 AA:  
 Query Match 95.6%; Score 346; DB 23; Length 67;  
 Best Local Similarity 97.0%; Pred. No. 3.5e-38;  
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 KGVSLPYRCPCRFESHVARANVKHLKILTPNCALQIVARLKNRRQVCIDPKLKWIOE 60  
 DB 1 KPVSLSYRCPCRFESHVARANVKHLKILTPNCALQIVARLKNRRQVCIDPKLKWIOE 60  
 QY 61 YLEKALN 67  
 DB 61 YLEKALN 67  
 DB 61 YLEKALN 67  
 RESULT 11  
 AAM50761  
 ID AAM50761 standard; peptide: 68 AA.  
 XX  
 AC AAM50761;  
 XX

XX  
 DT 27-JUL-1998 (first entry)  
 XX  
 DE Peptide which binds to CXCR4 receptor and is useful for treating HIV.  
 XX  
 KM Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus;  
 KM HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN FR2751658-A1.  
 PD  
 XX 30-JAN-1998.  
 PF  
 XX 26-JUL-1996; 96FR-0009477.  
 PR 26-JUL-1996; 96FR-0009477.  
 XX  
 PA (INSP ) INST PASTEUR.  
 PA  
 PI Arenzana SF, Baggiolini M, Clark LI, Moser B, Virelizier JL;  
 PI WPI; 1998-123039/12.  
 DR  
 XX  
 PT Human stromal cell-derived chemokine, SDF-1 - useful for treating  
 PT human immunodeficiency virus infection  
 PT  
 XX  
 PS Claim 5; Page 29; 48pp: French.  
 XX  
 CC The invention relates to peptides which bind to a cellular receptor for  
 CC CXCR4 chemokines, namely the CXCR4 receptor (also known as leukocyte-  
 CC expressed transmembrane domain receptor), especially where the  
 CC peptide is human chemokine SDF-1. The peptide can be used to treat or  
 CC prevent HIV infections, optionally together with reverse transcriptase  
 CC inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4  
 CC receptor antagonists, immunotherapy agents, agents for treating HIV-  
 CC associated opportunistic infections and/or other CXCR4 or CC chemokines,  
 CC especially RANTES, MIP-1 alpha, MIP-1 beta or MCP-1. The peptide can be  
 CC used to detect anti-SDF-1 antibodies in biological fluids. This  
 CC sequence represents a specifically claimed peptide which binds to the  
 CC CXCR4 receptor.  
 CC  
 XX  
 SQ Sequence 68 AA:  
 Query Match 95.6%; Score 346; DB 19; Length 68;  
 Best Local Similarity 97.0%; Pred. No. 3.6e-38;  
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 KGVSLPYRCPCRFESHVARANVKHLKILTPNCALQIVARLKNRRQVCIDPKLKWIOE 60  
 DB 2 KPVSLSYRCPCRFESHVARANVKHLKILTPNCALQIVARLKNRRQVCIDPKLKWIOE 61  
 QY 61 YLEKALN 67  
 DB 62 YLEKALN 68  
 DB 62 YLEKALN 68  
 RESULT 12  
 AAY05818  
 ID AAY05818 standard; Protein: 69 AA.  
 XX  
 AC AAY05818;  
 XX  
 DT 02-AUG-1999 (first entry)  
 XX  
 DE N-terminal modified chemokine met-hsDF-1 alpha.  
 XX  
 KM Stromal cell-derived factor 1 alpha; SDF-1 alpha; met-hsDF-1 alpha;  
 KM human; protein engineering; amino-terminal modification; mutant;  
 KM HIV; infection; angiogenesis; autoimmune disease; inflammation;  
 KM antiangiogenic; antiinflammatory; immunosuppressive; therapy;  
 KM vaccine.  
 XX

OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO9920759-A1.  
 XX  
 PD 29-APR-1999.  
 XX  
 PF 21-OCT-1998; 98WO-US22282.  
 XX  
 PR 20-OCT-1998; 98US-0175713.  
 PR 22-OCT-1997; 97US-095826.  
 PR 27-FEB-1998; 98WO-US04002.  
 XX  
 PA (GENY ) GENETICS INST INC.  
 XX  
 PI Herrmann SH, Lu Z, McCoy JM, Swanberg SL, Walker B;  
 PI Yang O;  
 DR WPI: 1999-288307/24.  
 DR N-PSDB; AAX25530.  
 XX  
 PT Modified chemokines useful for inhibiting or stimulating  
 PT angiogenesis  
 PS Claim 6c: Page 79; 85pp; English.  
 XX  
 CC The present sequence represents met-hsDF-1 alpha, i.e. human  
 CC stromal cell derived growth factor-1 alpha having an added  
 CC N-terminal methionine residue. DNA encoding met-hsDF-1 alpha (see  
 CC AA225530) was produced by cloning an NdeI/XbaI-restricted hSDF-1  
 CC alpha PCR product into the E. coli expression vector pAL781  
 CC in-frame with an ATG codon. met-hsDF-1 alpha is an example of  
 CC novel N-terminal modified chemokines (see AA05818-21) that have at  
 CC least one Met residue, at least one aminoxy-pentane residue or at  
 CC least one GroHEK peptide (see AA05822) covalently attached at the  
 CC C-terminus. The N-terminal modified chemokines are useful for  
 CC altering receptor function, inhibiting interactions between  
 CC chemokine receptors and their ligands. They are used as research  
 CC tools for identifying chemokine receptors, as vaccine adjuvants, as  
 CC agents for the chemotactic recruitment of migratory cells, as agents  
 CC for the stimulation or inhibition of angiogenesis, as agents against  
 CC autoimmune diseases and inflammation, and as agents to inhibit the  
 CC binding of HIV to certain receptors and the infection of  
 CC susceptible cells by HIV. HIV infection is best treated with  
 CC modified SDF-1 alpha and beta or MIP-1 alpha and beta.  
 CC  
 XX Sequence 69 AA;  
 SO  
 Query Match 95.6%; Score 346; DB 20; Length 69;  
 Best Local Similarity 97.0%; Pred. No. 3.7e-38;  
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 KGVSLPYRCPGRFFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 DB 2 KPVSLSYRCPGRFFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 61  
 OY 61 YLEKALN 67  
 DB 62 YLEKALN 68  
 DB  
 RESULT 13  
 AAW50762  
 ID AAW50762 standard; peptide; 72 AA.  
 XX  
 XX AAW50762;  
 AC  
 DT 27-JUL-1998 (first entry)  
 XX  
 XX Peptide which binds to CXCR4 receptor and is useful for treating HIV.  
 DE Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus;  
 XX HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.  
 KW

XX  
 OS Homo sapiens.  
 XX  
 PN FR2751658-A1.  
 XX  
 PD 30-JAN-1998.  
 XX  
 PF 26-JUL-1996; 96FR-0009477.  
 XX  
 PR 26-JUL-1996; 96FR-0009477.  
 PR 26-JUL-1996; 96FR-0009477.  
 XX  
 PA (INSP ) INST PASTEUR.  
 XX  
 PI Arenzana SF, Baggiolini M, Clark LI, Moser B, Virelizier JL;  
 PI WPI: 1998-123039/12.  
 DR  
 DR Human stromal cell-derived chemokine, SDF-1 - useful for treating  
 PT human immunodeficiency virus infection  
 PT  
 XX  
 PS Claim 5: Page 29; 48pp; French.  
 XX  
 CC The invention relates to peptides which bind to a cellular receptor for  
 CC CXCR4 chemokines, namely the CXCR4 receptor (also known as leukocyte-  
 CC expressed transmembrane domain receptor), especially where the  
 CC peptide is human chemokine SDF-1. The peptide can be used to treat or  
 CC prevent HIV infections, optionally together with reverse transcriptase  
 CC inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4  
 CC receptor antagonists, immunotherapy agents, agents for treating HIV-  
 CC associated opportunistic infections and/or other CXC or CC chemokines,  
 CC especially RANTES, MIP-1 alpha, MIP-1 beta or MCP-1. The peptide can be  
 CC used to detect anti-SDF-1 antibodies in biological fluids. This  
 CC sequence represents a specifically claimed peptide which binds to the  
 CC CXCR4 receptor.  
 CC  
 XX Sequence 72 AA;  
 SO  
 Query Match 95.6%; Score 346; DB 19; Length 72;  
 Best Local Similarity 97.0%; Pred. No. 3.9e-38;  
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 KGVSLPYRCPGRFFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 DB 1 KPVSLSYRCPGRFFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 OY 61 YLEKALN 67  
 DB 61 YLEKALN 67  
 DB  
 RESULT 14  
 AAY34093  
 ID AAY34093 standard; protein; 72 AA.  
 XX  
 XX AAY34093;  
 AC  
 DT 29-NOV-1999 (first entry)  
 XX  
 XX Native stromal cell derived factor 1 (SDF-1) beta protein.  
 DE  
 DE CXC chemokine receptor 4; CXCR4; antagonist; medicament; T-cell;  
 KW interferon gamma; autoimmune disease; multiple sclerosis; cancer;  
 KW angiogenesis; stromal cell derived factor 1; SDF-1.  
 XX  
 XX Mammalia.  
 OS  
 PN WO9947158-A2.  
 PN  
 PD 23-SEP-1999.  
 XX  
 PF 12-MAR-1999; 99WO-CA00221.  
 PR 13-MAR-1999; 98CA-2226391.  
 PR

PR 14-AUG-1998; 98CA-2245224.  
XX  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
PA  
XX Clark-Lewis I, Gong J, Duroonio V;  
PI  
XX WPI; 1999-561857/47.  
DR  
XX  
XX Use of CXC chemokine receptor 4 for treating autoimmune disease and  
PT cancer -  
XX  
XX Example 1: Fig 1: 71pp: English.  
PS  
XX  
XX The invention relates to the use of a CXC chemokine receptor 4 (CXCR4)  
CC antagonist for the manufacture of a medicament for reducing interferon  
CC gamma production by T-cells in a mammal. The CXCR4 antagonist can be used  
CC to treat or to design a medicament to treat, an autoimmune disease,  
CC multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4  
CC antagonists may be peptide compounds comprising a substantially purified  
CC peptide fragment, analogue or a pharmacologically acceptable salt of  
CC stromal cell derived factor 1 (SDF-1). The present sequence represents  
CC the amino acid sequence of SDF-1 beta protein.  
XX  
SQ Sequence 72 AA:  
Query Match 95.6%; Score 346; DB 20; Length 72;  
Best Local Similarity 97.0%; Pred. No. 3.9e-38;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 KGVSLPYRCPCRFESHVARANKHKLINTPNCALQIVARLKNNNQVCIDPKLKWIOE 60  
Db 1 KPVSLSYRCPCRFESHVARANKHKLINTPNCALQIVARLKNNNQVCIDPKLKWIOE 60  
QY 61 YLEKALN 67  
Db 61 YLEKALN 67  
RESULT 15  
AAV67595  
ID AAV67595 standard; peptide: 72 AA.  
XX  
XX AAV67595;  
AC  
XX  
XX 13-JUN-2000 (first entry)  
DT  
XX  
XX SDF-1beta peptide sequence.  
DE  
XX  
XX SDF-1; CXCR4; CXC chemokine receptor 4; gamma-interferon; cancer; gout;  
KW autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;  
KW type 1 diabetes; ulcerative colitis; lupus; antagonist; antitumour;  
KW stromal cell derived factor one; anti-inflammatory; immunomodulatory.  
XX  
XX Unidentified.  
OS  
XX  
XX W0200009152-A1.  
PN  
XX  
XX 24-FEB-2000.  
PD  
XX  
XX 16-AUG-1999; 99WO-CA00750.  
PF  
XX  
XX 14-AUG-1998; 98CA-2245224.  
PR  
XX  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
PA  
XX Clark-Lewis I, Gong J, Duroonio V, Salari H;  
PI  
XX WPI; 2000-224175/19.  
DR  
XX  
XX Therapeutic composition containing CXCR4 antagonist, useful for  
PT treating autoimmune disease, especially multiple sclerosis and cancer  
PT  
XX

PS Disclosure; Fig 1; 88pp; English.  
XX  
XX The invention provides a therapeutic composition containing an antagonist  
CC of CXCR4 (CXC chemokine receptor 4) and an excipient. The compositions  
CC are specifically used: to reduce production of gamma-interferon by T  
CC cells, particularly for treating autoimmune disease, especially multiple  
CC sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral  
CC sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative  
CC colitis, gout, lupus and transplant rejection; to treat cancer by  
CC inhibiting angiogenesis; inhibition of restenosis; and when labeled, to  
CC evaluate in vivo pharmacokinetics, or to determine disease progression  
CC and susceptibility, or as targeting agents for delivery of other  
CC therapeutic agents. The antagonist is selected from SDF-1 (stromal cell  
CC derived factor one) peptide fragments, SDF-1 being the only known natural  
CC ligand for CXCR4. The present sequence represents a SDF-1beta  
XX peptide sequence.  
XX  
SQ Sequence 72 AA:  
Query Match 95.6%; Score 346; DB 21; Length 72;  
Best Local Similarity 97.0%; Pred. No. 3.9e-38;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 KGVSLPYRCPCRFESHVARANKHKLINTPNCALQIVARLKNNNQVCIDPKLKWIOE 60  
Db 1 KPVSLSYRCPCRFESHVARANKHKLINTPNCALQIVARLKNNNQVCIDPKLKWIOE 60  
QY 61 YLEKALN 67  
Db 61 YLEKALN 67

Search completed: January 23, 2003, 15:33:42  
Job time : 28.2 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:33:47 ; Search time 9.8 seconds  
(without alignments)  
201.157 Million cell updates/sec

Title: US-09-852-424-3

Perfect score: 362  
Sequence: 1 KGVSLPYRCPCRFESHVAR.....QVCIDPKLKIOWIELEKALN 67

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/6C.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	346	95.6	89	1	US-08-323-084A-1
2	346	95.6	89	1	US-08-674-008-1
3	346	95.6	93	1	US-08-323-084A-5
4	346	95.6	93	1	US-08-674-008-5
5	346	95.6	326	3	US-08-808-720-3
6	346	95.6	328	3	US-08-808-720-1
7	345	95.3	79	1	US-08-181-556-2
8	96.5	26.7	99	2	US-08-436-420-25
9	96.5	26.7	99	1	US-08-352-324A-6
10	96.5	26.7	99	2	US-08-862-607-6
11	96.5	26.7	99	2	US-08-468-819-3
12	96.5	26.7	99	3	US-09-203-235-6
13	96.5	26.7	99	4	US-08-679-493A-150
14	96.5	26.7	99	5	PCT-US95-16144-6
15	96.5	26.7	99	6	Sequence 150, App1
16	94.5	26.1	70	1	US-08-330-163-24
17	94.5	26.1	70	1	US-08-482-111-24
18	94	26.0	67	1	US-08-244-702-12
19	94	26.0	67	1	US-08-244-702-14
20	94	26.0	68	1	US-08-244-702-9
21	94	26.0	68	1	US-08-244-702-10
22	94	26.0	68	1	US-08-244-702-11
23	94	26.0	69	1	US-08-244-702-2
24	94	26.0	69	1	US-08-244-702-8
25	94	26.0	72	1	US-07-956-863-1
26	94	26.0	72	1	US-07-778-413E-16
27	94	26.0	72	1	US-08-340-102-16

28	94	26.0	72	1	US-08-330-163-1	Sequence 1, App1
29	94	26.0	72	1	US-08-244-702-1	Sequence 1, App1
30	94	26.0	72	1	US-08-482-111-1	Sequence 1, App1
31	94	26.0	72	1	US-08-202-989-1	Sequence 1, App1
32	94	26.0	72	5	PCT-US94-02051-1	Sequence 1, App1
33	94	26.0	73	1	US-08-482-111-69	Sequence 69, App1
34	94	26.0	73	4	US-09-384-302A-26	Sequence 26, App1
35	94	26.0	76	2	US-08-468-819-79	Sequence 79, App1
36	94	26.0	76	2	US-08-468-819-81	Sequence 81, App1
37	92	25.4	64	1	US-08-330-163-21	Sequence 21, App1
38	92	25.4	64	1	US-08-482-111-21	Sequence 21, App1
39	92	25.4	71	3	US-08-615-232A-8	Sequence 8, App1
40	92	25.4	71	3	US-08-470-323-8	Sequence 8, App1
41	91.5	25.3	72	3	US-08-846-966-1	Sequence 1, App1
42	91.5	25.3	72	3	US-08-557-142-1	Sequence 1, App1
43	91.5	25.3	72	4	US-09-467-160-1	Sequence 1, App1
44	91.5	25.3	72	4	US-09-513-153-1	Sequence 1, App1
45	91.5	25.3	72	4	US-09-467-155-1	Sequence 1, App1

#### ALIGNMENTS

RESULT 1  
US-08-323-084A-1  
; Sequence 1, Application US/08323084A  
; Patent No. 5563048  
; GENERAL INFORMATION:  
; APPLICANT: HONJO, TASUKU  
; APPLICANT: SHIROZU, MICHIO  
; APPLICANT: TADA, HIDEAKI  
; TITLE OF INVENTION: No. 5563048el Polypeptides and DNAs encoding them  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SUGHRUE, MIOT, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20037-3202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/323,084A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 280505/1993  
; FILING DATE: 14-OCT-1993  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)293-7060  
; TELEFAX: (202)293-7860  
; TELEX: 6491103  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 89 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-323-084A-1

Query Match 95.6%; Score 346; DB 1; Length 89;

Best local Similarity 97.0%; Pred. No. 7e-38;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLPYRCPCRFESHVARANKHLKILTPNCALDIYARLKNRQVCIDPKLKWIOE 60  
DB 22 KPVSLPYRCPCRFESHVARANKHLKILTPNCALDIYARLKNRQVCIDPKLKWIOE 81  
QY 61 YLEKALN 67

Db 82 YLEKALN 88

## RESULT 2

US-08-674-008-1  
; Sequence 1, Application US/08674008  
; Patent No. 5756084  
; GENERAL INFORMATION:  
; APPLICANT: HONJO, Tasuku  
; APPLICANT: SHIROZU, Michio  
; TITLE OF INVENTION: HUMAN STROMAL DERIVED  
; TITLE OF INVENTION: FACTOR 1' AND 1 (As Amended)  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20037-3202  
; TELEPHONE: (202)293-7060  
; TELEFAX: (202)293-7860  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/674,008  
; FILING DATE: 1-JUL-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/323,084  
; FILING DATE: 14-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 280505/1993  
; FILING DATE: 14-OCT-1993  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)293-7060  
; TELEFAX: (202)293-7860  
; TELEX: 6491103  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 89 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-674-008-1

Query Match 95.6%; Score 346; DB 1; Length 89;  
Best Local Similarity 97.0%; Pred. No. 7e-38;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 KVSLSYRCPCRFESHVARANKHLKILTPNCALQIVARLKNKNNOVCIDPKLKWIOE 60  
Db 22 KVSLSYRCPCRFESHVARANKHLKILTPNCALQIVARLKNKNNOVCIDPKLKWIOE 81  
OY 61 YLEKALN 67  
Db 82 YLEKALN 88

## RESULT 3

US-08-323-084A-5  
; Sequence 5, Application US/08323084A  
; Patent No. 5563048  
; GENERAL INFORMATION:  
; APPLICANT: HONJO, TASUKU  
; APPLICANT: SHIROZU, MICHIO  
; TITLE OF INVENTION: No. 5563048e1 Polypeptides and DNAs encoding them  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20037-3202  
; TELEPHONE: (202)293-7060  
; TELEFAX: (202)293-7860  
; TELEX: 6491103  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 93 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-323-084A-5

Query Match 95.6%; Score 346; DB 1; Length 93;  
Best Local Similarity 97.0%; Pred. No. 7.3e-38;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KVSLSYRCPCRFESHVARANKHLKILTPNCALQIVARLKNKNNOVCIDPKLKWIOE 60  
Db 22 KVSLSYRCPCRFESHVARANKHLKILTPNCALQIVARLKNKNNOVCIDPKLKWIOE 81  
OY 61 YLEKALN 67  
Db 82 YLEKALN 88

## RESULT 4

US-08-674-008-5  
; Sequence 5, Application US/08674008  
; Patent No. 5756084  
; GENERAL INFORMATION:  
; APPLICANT: HONJO, Tasuku  
; APPLICANT: SHIROZU, Michio  
; TITLE OF INVENTION: HUMAN STROMAL DERIVED  
; TITLE OF INVENTION: FACTOR 1' AND 1 (As Amended)  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20037-3202  
; TELEPHONE: (202)293-7060  
; TELEFAX: (202)293-7860  
; TELEX: 6491103  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 93 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-674-008-5



PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: JP 280505/1993  
: FILING DATE: 14-OCT-1993  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (202)293-7060  
: TELEFAX: (202)293-7860  
: TELEX: 6491103  
: INFORMATION FOR SEQ ID NO: 5:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 93 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: US-08-674-008-5

Query Match 95.6%; Score 346; DB 1; Length 93;  
Best Local Similarity 97.0%; Pred. No. 7.3e-38;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLPYRCPGCFEFESHVARANVKHLKITLNPNCALQIVARLKNNNROVCDIPKIKWIOE 60  
DB 22 KPVSLSTYRCPGCFEFESHVARANVKHLKITLNPNCALQIVARLKNNNROVCDIPKIKWIOE 81  
OY 61 YLEKALN 67  
DB 82 YLEKALN 88

RESULT 5  
US-08-808-720-3  
: Sequence 3, Application US/08808720  
: Patent No. 6100387  
: GENERAL INFORMATION:  
: APPLICANT: Herrmann, Steve  
: APPLICANT: Swanberg, Stephen  
: TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING  
: TITLE OF INVENTION: CHEMOKINE DOMAINS  
: NUMBER OF SEQUENCES: 10  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Genetics Institute, Inc.  
: STREET: 87 Cambridgepark  
: CITY: Cambridge  
: STATE: MA  
: COUNTRY: USA  
: ZIP: 02140  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/808.720  
: FILING DATE:  
: CLASSIFICATION: 530  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Sprunger, Suzanne  
: REGISTRATION NUMBER: P-41,323  
: REFERENCE/DOCKET NUMBER: G15291  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (617) 498-8284  
: TELEFAX: (617) 876-5851  
: INFORMATION FOR SEQ ID NO: 3:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 326 amino acids  
: TYPE: amino acid  
: STRANDEDNESS:  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: US-08-808-720-3

Query Match 95.6%; Score 346; DB 3; Length 326;  
Best Local Similarity 97.0%; Pred. No. 3.2e-37;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLPYRCPGCFEFESHVARANVKHLKITLNPNCALQIVARLKNNNROVCDIPKIKWIOE 60  
DB 20 KPVSLSTYRCPGCFEFESHVARANVKHLKITLNPNCALQIVARLKNNNROVCDIPKIKWIOE 79  
OY 61 YLEKALN 67  
DB 80 YLEKALN 86

RESULT 6  
US-08-808-720-1  
: Sequence 1, Application US/08808720  
: Patent No. 6100387  
: GENERAL INFORMATION:  
: APPLICANT: Herrmann, Steve  
: APPLICANT: Swanberg, Stephen  
: TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING  
: TITLE OF INVENTION: CHEMOKINE DOMAINS  
: NUMBER OF SEQUENCES: 10  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Genetics Institute, Inc.  
: STREET: 87 Cambridgepark  
: CITY: Cambridge  
: STATE: MA  
: COUNTRY: USA  
: ZIP: 02140  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/808.720  
: FILING DATE:  
: CLASSIFICATION: 530  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Sprunger, Suzanne  
: REGISTRATION NUMBER: P-41,323  
: REFERENCE/DOCKET NUMBER: G15291  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (617) 498-8284  
: TELEFAX: (617) 876-5851  
: INFORMATION FOR SEQ ID NO: 1:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 328 amino acids  
: TYPE: amino acid  
: STRANDEDNESS:  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: US-08-808-720-1

Query Match 95.6%; Score 346; DB 3; Length 328;  
Best Local Similarity 97.0%; Pred. No. 3.3e-37;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLPYRCPGCFEFESHVARANVKHLKITLNPNCALQIVARLKNNNROVCDIPKIKWIOE 60  
DB 22 KPVSLSTYRCPGCFEFESHVARANVKHLKITLNPNCALQIVARLKNNNROVCDIPKIKWIOE 81  
OY 61 YLEKALN 67  
DB 82 YLEKALN 88

RESULT 7  
US-08-181-556-2  
: Sequence 2, Application US/08181556  
: Patent No. 5523486  
: GENERAL INFORMATION:  
: APPLICANT: HONJO, Tasuku  
: APPLICANT: TASHIRO, Kei  
: APPLICANT: TADA, Hideaki



INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-352-324A-6

Query Match 26.7%: Score 96.5; DB 1; Length 99;  
Best Local Similarity 31.1%: Pred. No. 2.3e-05;  
Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5;

QY 1 KGVSLP-----YRCPC-REFESHVARANKHLKILNT-PNCA-LQIVARLKNNROVCID 52  
DB 21 EGAVLPBSAKELRCQCICKYKSPFHPKFIKELRVIESGPHCANTETIIVKL-SGGRLECID 79  
QY 53 PKIKWQIETLEKAL 66  
DB 80 PKNWQVRVEKFL 93

## RESULT 10

US-08-862-607-6  
Sequence 6, Application US/08862607  
Patent No. 5844084  
GENERAL INFORMATION:  
APPLICANT: Guegler, Karl J.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Wilde, Craig G.  
APPLICANT: Selhammer, Jeffrey J.  
TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN  
TITLE OF INVENTION: INFLAMED ADENOID, ITS PRODUCTION AND USES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: US  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/862,607  
FILING DATE: 23-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/352,324  
FILING DATE: 07-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0025 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-862-607-6

Query Match 26.7%: Score 96.5; DB 2; Length 99;  
Best Local Similarity 31.1%: Pred. No. 2.3e-05;  
Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5;

QY 1 KGVSLP-----YRCPC-REFESHVARANKHLKILNT-PNCA-LQIVARLKNNROVCID 52  
DB 21 EGAVLPBSAKELRCQCICKYKSPFHPKFIKELRVIESGPHCANTETIIVKL-SGGRLECID 79  
QY 53 PKIKWQIETLEKAL 66  
DB 80 PKNWQVRVEKFL 93

## RESULT 11

US-08-468-819-3  
Sequence 3, Application US/08468819  
Patent No. 5871723  
GENERAL INFORMATION:  
APPLICANT: Strieter, Robert M.  
APPLICANT: Polverini, Peter J.  
APPLICANT: Kunkel, Steven L.  
TITLE OF INVENTION: CXc Chemokines as Regulators of  
TITLE OF INVENTION: Angiogenesis  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: US  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,819  
FILING DATE: Concurrently herewith  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: UMIC:003/HYL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7477  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-468-819-3

Query Match 26.7%: Score 96.5; DB 2; Length 99;  
Best Local Similarity 31.1%: Pred. No. 2.3e-05;  
Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5;

QY 1 KGVSLP-----YRCPC-REFESHVARANKHLKILNT-PNCA-LQIVARLKNNROVCID 52  
DB 21 EGAVLPBSAKELRCQCICKYKSPFHPKFIKELRVIESGPHCANTETIIVKL-SGGRLECID 79  
QY 53 PKIKWQIETLEKAL 66  
DB 80 PKNWQVRVEKFL 93

## RESULT 12

US-09-203-235-6  
Sequence 6, Application US/09203235  
Patent No. 6071701  
GENERAL INFORMATION:  
APPLICANT: Guegler, Karl J.  
APPLICANT: Hawkins, Phillip R.

```

1 APPLICANT: Wilde, Craig G.
2 APPLICANT: Seilhamer, Jeffrey J.
3 TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN
4 TITLE OF INVENTION: INFLAMED ADENOID, ITS PRODUCTION AND USES
5 NUMBER OF SEQUENCES: 9
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Incyte Pharmaceuticals, Inc.
8 STREET: 3174 Porter Drive
9 CITY: Palo Alto
10 STATE: CA
11 COUNTRY: US
12 ZIP: 94304
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Diskette
15 COMPUTER: IBM Compatible
16 OPERATING SYSTEM: DOS
17 SOFTWARE: FASTSEQ Version 1.5
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/09/203,235
20 FILING DATE:
21 CLASSIFICATION:
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: 08/862,607
24 FILING DATE: 23-MAY-1997
25 APPLICATION NUMBER: 08/352,324
26 FILING DATE: 07-DEC-1994
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Luther, Barbara J.
29 REGISTRATION NUMBER: 33,954
30 REFERENCE/DOCKET NUMBER: PF-0025 US
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: 415-855-0555
33 TELEFAX: 415-852-0195
34 INFORMATION FOR SEQ ID NO: 6:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 99 amino acids
37 TYPE: amino acid
38 STRANDEDNESS: single
39 TOPOLOGY: linear
40 MOLECULE TYPE: peptide
41 US-09-203-235-6
42
43 Query Match 26.7%; Score 96.5; DB 3; Length 99;
44 Best Local Similarity 31.1%; Pred. No. 2.3e-05;
45 Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5
46
47 QY 1 KGVSLP-----YRCPG-RFFESHVARANKHLKILNT-PNCA-LQIVARKNNROYCID 52
48 : : || : : : : : : : : : : : : : : : : : : : : : : : : : :
49 Db 21 EGAVLPRAKAKELRCGCITKYSKPFHPKFIKELRVIESGHCANTETIVVL-SDGRRLCID 79
50 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
51 QY 53 PKLWIOEYLEKAL 66
52 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
53 Db 80 KPNMNVQRVVERKFL 93
54
55 RESULT 13
56 US-08-679-493A-150
57 Sequence 150, Application US/08679493A
58 Patent No. 6303295
59 GENERAL INFORMATION:
60 APPLICANT: Taylor, Ethan W.
61 TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
62 FILE REFERENCE: 55-95
63 CURRENT APPLICATION NUMBER: US/08/679,493A
64 CURRENT FILING DATE: 1996-07-12
65 PRIOR APPLICATION NUMBER: 60/001203
66 PRIOR FILING DATE: 1995-07-14
67 PRIOR APPLICATION NUMBER: 60/003,112
68 PRIOR FILING DATE: 1995-09-01
69 NUMBER OF SEQ ID NOS: 216
70 SOFTWARE: PatentIn Ver. 2.0
71 SEQ ID NO 150
72 LENGTH: 99

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-679-493A-150

Query Match
Best Local Similarity 26.7%; Score 96.5; DB 4; Length 99;
Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5

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       :| ||           || | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      21 EGAVLPKRAKELRCCCKITKYSPFHPRFIKEHLVIESGPHCANTELIIYKL-SDGRELCID 79

Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5

OY      53 PKLKWIOEYLEKAL 66
       || | :| :| :|
Db      80 PRENVQVRVERKFL 93

RESULT 14
PCT-US95-16144-6
; Sequence 6, Application PC/TUS9516144
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN INFAMED
; TITLE OF INVENTION: ADENOID, ITS PRODUCTION AND USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16144
FILING DATE: 07-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,324
FILING DATE: 07-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PF-0025 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-16144-6

Query Match
Best Local Similarity 26.7%; Score 96.5; DB 5; Length 99;
Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5

OY      1 KGVSLP-----YRCPC-RFESHVARAVNKHILKIINT-PNCA-LQIVARLKNNNQVCID 52
       :| ||           || | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      21 EGAVLPKRAKELRCCCKITKYSPFHPRFIKEHLVIESGPHCANTELIIYKL-SDGRELCID 79

Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5

OY      53 PKLKWIOEYLEKAL 66
       || | :| :| :|
Db      80 PRENVQVRVERKFL 93

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RESULT 15
5451399-2
; Patent No. 5451399
; APPLICANT: GIMBRINE, MICHAEL A.; OBIN, MARTIN S.; BAKER,
; JOFFRE, B.; HEBERT, CAROLINE A.
; TITLE OF INVENTION: (ALA IL-8)77 AND (SER IL-8)72 AS
; LEUKOCYTE ADHESION INHIBITORS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/964,525
; FILING DATE: 19-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 443,131
; FILING DATE: 29-NOV-1989
; SEQ ID NO:2:
; LENGTH: 99
5451399-2

Query Match          26.7%; Score 96.5; DB 6; Length 99;
Best Local Similarity 31.1%; Pred No. 2,3e-05;
Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5;

Qy 1 KGVSLP-----YRCP-REFESHVARANYKHLKILNT-PNCA-LQIVARLKNNNQVCID 52
   : 1 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 21 ECAVLPRSAKELRCQICKTKYSKPFHPKFIKELRVIESGPHCANTEIIVKL-SDGRELCID 79
   : 1 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 53 PKLKIQOEYLEKAL 66
   11 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 80 PKNWVQRVVEKFL 93
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Search completed: January 23, 2003, 15:38:58  
Job time : 10.8 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:31:18 ; Search time 6.2 Seconds  
(without alignments)  
218.059 Million cell updates/sec

Title: US-09-852-424-3

Perfect score: 362  
Sequence: 1 KGVSLPYRCRCRFESHVAR.....QVCIDPKLKIQVLEKALN 67

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	362	100.0	67	9	US-09-852-424-3
2	354	97.8	67	9	US-09-852-424-1
3	353	97.5	67	9	US-09-852-424-7
4	349	96.4	67	9	US-09-852-424-6
5	348	96.1	67	9	US-09-852-424-9
6	347	95.9	67	9	US-09-852-424-2
7	347	95.9	67	9	US-09-852-424-5
8	346	95.6	67	9	US-09-852-424-8
9	346	95.6	67	9	US-09-835-107-1
10	346	95.6	67	10	US-09-144-838-8
11	346	95.6	67	10	US-09-144-838-23
12	346	95.6	89	8	US-08-927-939-22
13	346	95.6	89	9	US-09-792-793A-32
14	346	95.6	89	10	US-09-953-692-4
15	346	95.6	89	10	US-09-953-717-4
16	346	95.6	93	8	US-08-927-939-56
17	346	95.6	93	8	US-09-835-107-2
18	346	95.6	93	9	US-09-835-107-3
19	346	95.6	93	9	US-09-792-793A-93

20	346	95.6	93	10	US-09-144-838-7	Sequence 7, Appl
21	346	95.6	93	10	US-09-919-497-95	Sequence 95, Appl
22	346	95.6	320	9	US-09-792-793A-77	Sequence 77, Appl
23	346	95.6	322	9	US-09-792-793A-78	Sequence 78, Appl
24	346	95.6	327	9	US-09-792-793A-79	Sequence 79, Appl
25	344	95.0	67	9	US-09-852-424-4	Sequence 4, Appl
26	339.5	93.8	66	9	US-09-852-424-10	Sequence 10, Appl
27	336.5	93.0	66	9	US-09-852-424-11	Sequence 11, Appl
28	330.5	91.3	66	9	US-09-852-424-12	Sequence 12, Appl
29	328.5	90.7	66	10	US-09-144-838-27	Sequence 27, Appl
30	320.5	88.5	68	10	US-09-144-838-51	Sequence 51, Appl
31	304	84.0	68	10	US-09-144-838-47	Sequence 47, Appl
32	295	81.5	68	10	US-09-144-838-24	Sequence 24, Appl
33	292	80.7	67	10	US-09-144-838-25	Sequence 25, Appl
34	277.5	76.7	67	10	US-09-144-838-28	Sequence 28, Appl
35	269.5	74.4	69	10	US-09-144-838-52	Sequence 52, Appl
36	266.5	73.6	68	10	US-09-144-838-53	Sequence 53, Appl
37	254.5	70.3	66	10	US-09-144-838-29	Sequence 29, Appl
38	253	69.9	68	10	US-09-144-838-48	Sequence 48, Appl
39	250	69.1	67	10	US-09-144-838-49	Sequence 49, Appl
40	241	66.6	68	10	US-09-144-838-26	Sequence 26, Appl
41	223.5	61.7	67	10	US-09-144-838-30	Sequence 30, Appl
42	223	61.6	67	10	US-09-144-838-31	Sequence 31, Appl
43	215.5	59.5	69	10	US-09-144-838-54	Sequence 54, Appl
44	212.5	58.7	66	10	US-09-144-838-35	Sequence 35, Appl
45	199	55.0	68	10	US-09-144-838-50	Sequence 50, Appl

#### ALIGNMENTS

```

RESULT 1
US-09-852-424-3
; Sequence 3, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
US-09-852-424-3

Query Match      100.0%; Score 362; DB 9; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.6e-33;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGVSLPYRCRCRFESHVARANKHKLINTPCALQIYARLKNRRQVCIDPKLWQE 60
      |||||||
DB      1 KGVSLPYRCRCRFESHVARANKHKLINTPCALQIYARLKNRRQVCIDPKLWQE 60
      |||||||
QY      61 YLEKALN 67
      |||||||
DB      61 YLEKALN 67
      |||||||

RESULT 2
US-09-852-424-1
; Sequence 1, Application US/09852424

```

Patent No. US20020156034A1  
GENERAL INFORMATION:  
APPLICANT: The University of British Columbia; and  
TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: 80021-257  
CURRENT APPLICATION NUMBER: US/09/852,424  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: CA 2,305,787  
PRIOR FILING DATE: 2000-05-09  
PRIOR APPLICATION NUMBER: US 60/205,467  
PRIOR FILING DATE: 2000-05-19  
NUMBER OF SEQ ID NOS: 135  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
US-09-852-424-1

Query Match 97.8%; Score 354; DB 9; Length 67;  
Best Local Similarity 98.5%; Pred. No. 2,7e-32;  
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KGVSLLPYRCPCRFESHVARANVHKILTPNCALQIVARLKNNNQVCIIDPKLKWIOE 60  
Db 1 KGVSLLPYRCPCRFESHVARANVHKILTPNCALQIVARLKNNNQVCIIDPKLKWIOE 60  
QY 61 YLEKALN 67  
Db 61 YLEKALN 67

RESULT 3  
US-09-852-424-7  
Sequence 7, Application US/09852424  
Patent No. US20020156034A1

GENERAL INFORMATION:  
APPLICANT: The University of British Columbia; and  
APPLICANT: Chemokine Therapeutics Corporation  
TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: 80021-257  
CURRENT APPLICATION NUMBER: US/09/852,424  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: CA 2,305,787  
PRIOR FILING DATE: 2000-05-09  
PRIOR APPLICATION NUMBER: US 60/205,467  
PRIOR FILING DATE: 2000-05-19  
NUMBER OF SEQ ID NOS: 135  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MUTAGEN  
LOCATION: (6)  
OTHER INFORMATION: Xaa-P\*-proline-amino acid chimera. See page 17 of  
OTHER INFORMATION: disclosure for possible structures for P\*  
OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
OTHER INFORMATION: Laboratory  
US-09-852-424-7

Query Match 97.5%; Score 353; DB 9; Length 67;  
Best Local Similarity 98.5%; Pred. No. 3,4e-32;  
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KGVSLLPYRCPCRFESHVARANVHKILTPNCALQIVARLKNNNQVCIIDPKLKWIOE 60  
Db 1 KGVSLLPYRCPCRFESHVARANVHKILTPNCALQIVARLKNNNQVCIIDPKLKWIOE 60

QY 61 YLEKALN 67  
Db 61 YLEKALN 67

RESULT 4  
US-09-852-424-6  
Sequence 6, Application US/09852424  
Patent No. US20020156034A1  
GENERAL INFORMATION:  
APPLICANT: The University of British Columbia; and  
APPLICANT: Chemokine Therapeutics Corporation  
TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: 80021-257  
CURRENT APPLICATION NUMBER: US/09/852,424  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: CA 2,305,787  
PRIOR FILING DATE: 2000-05-09  
PRIOR APPLICATION NUMBER: US 60/205,467  
PRIOR FILING DATE: 2000-05-19  
NUMBER OF SEQ ID NOS: 135  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MUTAGEN  
LOCATION: (5)  
OTHER INFORMATION: Xaa-P\*-proline-amino acid chimera. See page 17 of  
OTHER INFORMATION: disclosure for possible structures for P\*  
OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
US-09-852-424-6

Query Match 96.4%; Score 349; DB 9; Length 67;  
Best Local Similarity 97.0%; Pred. No. 9,4e-32;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLLPYRCPCRFESHVARANVHKILTPNCALQIVARLKNNNQVCIIDPKLKWIOE 60  
Db 1 KGVSLLPYRCPCRFESHVARANVHKILTPNCALQIVARLKNNNQVCIIDPKLKWIOE 60  
QY 61 YLEKALN 67  
Db 61 YLEKALN 67

RESULT 5  
US-09-852-424-9  
Sequence 9, Application US/09852424  
Patent No. US20020156034A1  
GENERAL INFORMATION:  
APPLICANT: The University of British Columbia; and  
APPLICANT: Chemokine Therapeutics Corporation  
TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: 80021-257  
CURRENT APPLICATION NUMBER: US/09/852,424  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: CA 2,305,787  
PRIOR FILING DATE: 2000-05-09  
PRIOR APPLICATION NUMBER: US 60/205,467  
PRIOR FILING DATE: 2000-05-19  
NUMBER OF SEQ ID NOS: 135  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MUTAGEN  
LOCATION: (8)



OTHER INFORMATION: xaa-p\*-proline-amino acid chimera. See page 17 of  
OTHER INFORMATION: disclosure for possible structures for p\*  
OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
OTHER INFORMATION: Laboratory  
US-09-852-424-9

Query Match 96.1%; Score 348; DB 9; Length 67;  
Best Local Similarity 97.0%; Pred. No. 1.2e-31;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 KGVSLPYRCPCRFESHVARAVNKHKLINTPNCALQIVARLKNNNROYCIDPKLKWIOE 60  
|||||  
Db 1 KGVSLPYRCPCRFESHVARAVNKHKLINTPNCALQIVARLKNNNROYCIDPKLKWIOE 60

Oy 61 VLEKALN 67  
|||||  
Db 61 VLEKALN 67

RESULT 6  
US-09-852-424-2

Sequence 2, Application US/09852424  
Patent No. US20020156034A1

GENERAL INFORMATION:  
APPLICANT: The University of British Columbia; and  
APPLICANT: Chemokine Therapeutics Corporation  
TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: 80021-257  
CURRENT APPLICATION NUMBER: US/09/852,424  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: CA 2,305,787  
PRIOR FILING DATE: 2000-05-09  
PRIOR APPLICATION NUMBER: US 60/205,467  
PRIOR FILING DATE: 2000-05-19  
NUMBER OF SEQ ID NOS: 135  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
OTHER INFORMATION: Laboratory  
US-09-852-424-2

Query Match 95.9%; Score 347; DB 9; Length 67;  
Best Local Similarity 97.0%; Pred. No. 1.6e-31;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 KGVSLPYRCPCRFESHVARAVNKHKLINTPNCALQIVARLKNNNROYCIDPKLKWIOE 60  
|||||  
Db 1 KGVSLPYRCPCRFESHVARAVNKHKLINTPNCALQIVARLKNNNROYCIDPKLKWIOE 60

Oy 61 VLEKALN 67  
|||||  
Db 61 VLEKALN 67

RESULT 7  
US-09-852-424-5

Sequence 5, Application US/09852424  
Patent No. US20020156034A1

GENERAL INFORMATION:  
APPLICANT: The University of British Columbia; and  
APPLICANT: Chemokine Therapeutics Corporation  
TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: 80021-257  
CURRENT APPLICATION NUMBER: US/09/852,424  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: CA 2,305,787  
PRIOR FILING DATE: 2000-05-09  
PRIOR APPLICATION NUMBER: US 60/205,467  
PRIOR FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 135  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
OTHER INFORMATION: Laboratory  
US-09-852-424-5

Query Match 95.9%; Score 347; DB 9; Length 67;  
Best Local Similarity 97.0%; Pred. No. 1.6e-31;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 KGVSLPYRCPCRFESHVARAVNKHKLINTPNCALQIVARLKNNNROYCIDPKLKWIOE 60  
|||||  
Db 1 KGVSLPYRCPCRFESHVARAVNKHKLINTPNCALQIVARLKNNNROYCIDPKLKWIOE 60

Oy 61 VLEKALN 67  
|||||  
Db 61 VLEKALN 67

RESULT 8  
US-09-852-424-8

Sequence 8, Application US/09852424  
Patent No. US20020156034A1

GENERAL INFORMATION:  
APPLICANT: The University of British Columbia; and  
APPLICANT: Chemokine Therapeutics Corporation  
TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: 80021-257  
CURRENT APPLICATION NUMBER: US/09/852,424  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: CA 2,305,787  
PRIOR FILING DATE: 2000-05-09  
PRIOR APPLICATION NUMBER: US 60/205,467  
PRIOR FILING DATE: 2000-05-19  
NUMBER OF SEQ ID NOS: 135  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MUTAGEN  
LOCATION: (7)  
OTHER INFORMATION: xaa-p\*-proline-amino acid chimera. See page 17 of  
OTHER INFORMATION: disclosure for possible structures for p\*  
OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
OTHER INFORMATION: Laboratory  
US-09-852-424-8

Query Match 95.6%; Score 346; DB 9; Length 67;  
Best Local Similarity 97.0%; Pred. No. 2e-31;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 KGVSLPYRCPCRFESHVARAVNKHKLINTPNCALQIVARLKNNNROYCIDPKLKWIOE 60  
|||||  
Db 1 KGVSLPYRCPCRFESHVARAVNKHKLINTPNCALQIVARLKNNNROYCIDPKLKWIOE 60

Oy 61 VLEKALN 67  
|||||  
Db 61 VLEKALN 67

RESULT 9  
US-09-835-107-1

Sequence 1, Application US/09835107  
Patent No. US20020156123A1  
GENERAL INFORMATION:  
APPLICANT: Tudan, Christopher R.

```

APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: SDF-1 alpha
US-09-835-107-1

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Query Match          95.6%; Score 346; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 2e-31;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

OY 1 KGVSLPYRCPCHFFESHVARANVKHLKILTPNCALQIVARLKNNNRQYCIDPKLKWIOE 60
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1 KPVSLSYRCPCHFFESHVARANVKHLKILTPNCALQIVARLKNNNRQYCIDPKLKWIOE 60
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
OY 61 YLEKALN 67
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 61 YLEKALN 67
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 10
US-09-144-838-8
: Sequence 8, Application US/09144838A
: Patent No. US20020051996A1
: GENERAL INFORMATION:
: APPLICANT: Siahi, Michael A.
: APPLICANT: Wilken, Jill
: APPLICANT: Simon, Reyna
: APPLICANT: Kent, Stephen B.H.
: TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
: FILE REFERENCE: GRN-020/01US
: CURRENT APPLICATION NUMBER: US/09/144,838A
: CURRENT FILING DATE: 1998-08-31
: EARLIER APPLICATION NUMBER: US 60/057,620
: EARLIER FILING DATE: 1997-09-04
: NUMBER OF SEQ ID NOS: 54
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 8
: LENGTH: 67
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-144-838-8

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Query Match	95.6%	Score 346;	DB 10,	length 67;
Local Similarity	97.0%;	Pred. No. 2e-31;		
Matches	65;	Conservative	0;	Mismatches 2; Indels 0; Gaps 0.

Oy	1	KGVSLPYRCPCEFFESHAVARAVYKHLKLTINPNCALQIYARLKNNNROYCIDPKLKTIOE	60
	1		
	1		
1	KPVSLSYRCPCEFFESHAVARAVYKHLKLTINPNCALQIYARLKNNNROYCIDPKLKTIOE	60	

Qy	61	YLEKALN	67
Db	61	YLEKALN	67

```

: RESULT 11
: US-09-144-838-23
: Sequence 23, Application US/09144838A
: Patent No. US20020051996A1
: GENERAL INFORMATION:
: APPLICANT: Stani, Michael A.
: APPLICANT: Wilken, Jill
: APPLICANT: Simon, Reyna
: APPLICANT: Kent, Stephen B.H.
: TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
: FILE REFERENCE: GREN-020/01US
: CURRENT APPLICATION NUMBER: US/09/144,838A
: CURRENT FILING DATE: 1998-08-31
: EARLIER APPLICATION NUMBER: US 60/057,620
: EARLIER FILING DATE: 1997-09-04
: NUMBER OF SEQ. ID NOS: 54
: SOFTWARE: PatentIn Ver. 2.1
: SEQ. ID NO 23
: LENGTH: 67
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: US-09-144-838-23

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Query Match	95.6%	Score 346	DB 10	Length 67
Best Local Similarity	97.0%	Pred. No. 2e-31		
Matches	65	Conservative	0	Mismatches 2
				Indels 0
				Gaps 0
OY	1	KGVSIPYPCPCFEESHVARANVKHLKITLPNCALQIYARLKNNNROYCIDPKLWIOE	60	
	1			
Db	1	KPVSLSTYRCPCCFEESHVARANVKHLKITLPNCALQIYARLKNNNROYCIDPKLWIOE	60	
OY	61	YLEKALN	67	
	61			
Db	61	YLEKALN	67	

```

RESULT 12
US-08-927-939-22
; Sequence 22, Application US/08927939
; Patent No. US2001000640A1
; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Lauren Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; TITLE OF INVENTION: augment an inflammatory response.
; FILE REFERENCE: 295.022051
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-927-939-22

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Query Match	95.6%	Score 346;	DB 8;	Length 89;
Best Local Similarity	97.0%	Pred. No. 2.6e-31;		
Matches 65; Conservative	0; Mismatches 2;	Indels 0;	Gaps 0;	
Oy	1	KGVSIPYRCPCFEFESHARAVNKLILINPNCALQIYARLKNNNROYCIDPKLWIOE	60	
Db	22	KPVSLSYKPCPCFEFESHARAVNKLILINPNCALQIYARLKNNNROYCIDPKLWIOE	81	
Oy	61	YLEKALN	67	

DB 82 YLEKALN 88

RESULT 13

US-09-792-793A-32  
; Sequence 32, Application US/09792793A  
; Patent No. US20020168370A1  
; GENERAL INFORMATION:

APPLICANT: McDonald, John R.

APPLICANT: Coggin, Philip

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND

TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS

FILE REFERENCE: 25020-601D

CURRENT APPLICATION NUMBER: US/09/792,793A

NUMBER OF SEQ ID NOS: 93

SOFTWARE: Patent Ver. 2.0

SEQ ID NO 32

LENGTH: 89

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: OTHER INFORMATION: Human Chemokine Polypeptide: Stromal cell-derived

PUBLICATION INFORMATION: Factor-1-Alpha (SDF-1-Alpha)

JOURNAL: Genomics

VOLUME: 28

PAGES: 495-500

DATE: 1995

US-09-792-793A-32

Query Match

Best Local Similarity 97.0%; Score 346; DB 9; Length 89;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKIOE 60

DB 22 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKIOE 81

QY 61 YLEKALN 67

DB 82 YLEKALN 88

RESULT 14

US-09-953-692-4

; Sequence 4, Application US/09953692

; Patent No. US20020107195A1

; GENERAL INFORMATION:

APPLICANT: Shalley, Gupta K.

TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by

TITLE OF INVENTION: Administering Stromal Cell Derived Factor-1(

FILE REFERENCE: P50676C1

CURRENT APPLICATION NUMBER: US/09/953,692

CURRENT FILING DATE: 2001-09-17

PRIOR FILING DATE: 1998-07-21

PRIOR APPLICATION NUMBER: 60/093,596

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4

LENGTH: 89

TYPE: PRT

ORGANISM: Human

US-09-953-692-4

Query Match

Best Local Similarity 97.0%; Score 346; DB 10; Length 89;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 22 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKIOE 81

QY 61 YLEKALN 67

DB 82 YLEKALN 88

RESULT 15

US-09-953-717-4

; Sequence 4, Application US/09953717

; Patent No. US20020107196A1

; GENERAL INFORMATION:

APPLICANT: Shalley, Gupta K.

TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by

TITLE OF INVENTION: Administering Stromal Cell Derived Factor-1(

FILE REFERENCE: P50676D1

CURRENT APPLICATION NUMBER: US/09/953,717

CURRENT FILING DATE: 2001-09-17

PRIOR FILING DATE: 1998-07-21

PRIOR APPLICATION NUMBER: 60/093,596

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4

LENGTH: 89

TYPE: PRT

ORGANISM: Human

US-09-953-717-4

Query Match

Best Local Similarity 97.0%; Score 346; DB 10; Length 89;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKIOE 60

DB 22 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKIOE 81

QY 61 YLEKALN 67

DB 82 YLEKALN 88

Search completed: January 23, 2003, 15:38:01

Job time : 6.2 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:31:02 : Search time 11.6 Seconds

(without alignments)  
555.259 Million cell updates/sec

Title: US-09-852-424-3

Perfect score: 362  
Sequence: 1 KGVSLPRPCRFESHVAR.....QVCIDPKKMKIQLKALN 67

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: PIR.73:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	346	95.6	93	2	G01540
2	345	95.3	89	2	A53497
3	345	95.3	89	2	I53416
4	345	95.3	93	2	I81182
5	101	27.9	101	2	I48148
6	97	26.8	95	2	JN0841
7	96.5	26.7	99	2	A37034
8	92	25.4	101	2	S42496
9	92	25.4	120	2	I48147
10	91.5	25.3	96	2	A32954
11	91	25.1	91	1	A46539
12	91	25.1	103	2	A53096
13	89	24.6	120	2	J60177
14	89	24.6	148	1	A30209
15	89	24.6	148	1	S07723
16	87.5	24.2	96	2	JN0572
17	87	24.0	101	2	I46871
18	86	23.8	91	1	A28815
19	84.5	23.1	100	2	JH0200
20	83.5	22.1	92	2	I53322
21	82.5	22.5	75	2	A54188
22	81.5	22.8	75	2	B54188
23	81.5	22.5	119	2	S42881
24	80.5	22.2	96	2	I48099
25	80	22.1	109	2	A54678
26	79.5	22.0	100	2	S21467
27	79.5	22.0	100	2	I55614
28	79.5	22.0	107	2	B38290
29	78.5	21.7	107	2	A28414

## ALIGNMENTS

30	78.5	21.7	132	2	A57325	C-X-C chemokine LI
31	78	21.5	96	2	JC2478	ectoxin precursor
32	77.5	21.4	101	2	B28414	growth-regulated p
33	77.5	21.4	114	2	A55010	neutrophil-activat
34	77.5	21.4	117	2	B44253	alveolar macrophag
35	76.5	21.1	103	2	A26736	transformation-ind
36	76.5	21.1	103	2	I50417	RSV-induced protei
37	75.5	20.9	870	2	A41130	dysostrophin homolo
38	74	20.4	125	2	I46857	monocyte chemoattr
39	73.5	20.3	107	2	JH0281	macrophage inflamm
40	73	20.2	92	2	A32393	macrophage inflamm
41	72.5	20.0	126	2	A35766	platelet factor 4,
42	71.5	19.8	128	1	TCGU	beta-thromboglobul
43	71	19.6	99	2	JC5295	monocyte chemoattr
44	70.5	19.5	53	2	I64831	gene KC protein -
45	69.5	19.2	104	1	PFH04A	platelet factor 4

RESULT 1  
G01540  
cytokine SDF-1-beta - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 26-Aug-1999  
C:Accession: G01540  
R:Spotila, L.D.  
submitted to the EMBL Data Library, October 1994  
A:Reference number: G07697  
A:Accession: G01540  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-93 <SPO>  
A:Cross-references: EMBL:016752; NID:q1272194; PID:9571508  
C:Superfamily: beta-thromboglobulin

Query Match 95.6% Score 346; DB 2; Length 93;  
Best Local Similarity 97.0% Pred. No. 4.5e-35;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLPRPCRFESHVARVANKHLKLTNPNCALQIVARLKNNNRQVCIDPKKMKIOWE 60  
DB 22 KGVSLPRPCRFESHVARVANKHLKLTNPNCALQIVARLKNNNRQVCIDPKKMKIOWE 81

QY 61 YLEKALN 67  
DB 82 YLEKALN 88

RESULT 2  
A53497  
pre-B-cell growth-stimulating factor precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 20-Jun-2000  
C:Accession: A53497; I59582  
R:Nagesawa, T.; Kikutan, H.; Kishimoto, T.  
Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994  
A:Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.  
A:Reference number: A53497; MUID:94181581; PMID:8134392  
A:Accession: A53497  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-89 <NAG>  
A:Cross-references: GB:D21072; NID:9413905; PIDN:BAA04648.1; PID:9468457  
R:Tashiro, K.; Tada, H.; Heliker, R.; Shirozu, M.; Nakano, T.; Honjo, T.  
Science 261, 600-603, 1993  
A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I me  
A:Reference number: I59582; MUID:93542488; PMID:8342023  
A:Accession: I59582  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-89 <RES>

A:Cross-references: GB:L12029; NID:g393179; PIDN:AAA40100.1; PID:g393180  
C:Genetics:  
A:Gene: SDF-1-alpha  
C:Superfamily: beta-thromboglobulin  
C:Keywords: cytokine

Query Match 95.3%; Score 345; DB 2; Length 89;  
Best Local Similarity 95.5%; Pred. No. 5.7e-35;  
Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
DB 22 KPVSLSRCCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81  
QY 61 YLEKALN 67  
DB 82 YLEKALN 88

#### RESULT 3

Interleukin-8 homolog - mouse

C:Species: Mus sp. (mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I53416  
R:Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.  
Exp. Cell Res. 215, 284-293, 1994  
A:Title: Molecular cloning of TPRL1, a gene whose expression is repressed by the tumor  
A:Reference number: I53416; MUID:95073437; PMID:7982471  
A:Accession: I53416  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-89 <RES>  
A:Cross-references: GB:S74318; NID:g786393; PIDN:AA32650.1; PID:g786394  
C:Genetics:  
A:Gene: TPRL1  
C:Superfamily: beta-thromboglobulin

Query Match 95.3%; Score 345; DB 2; Length 89;  
Best Local Similarity 95.5%; Pred. No. 5.7e-35;  
Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
DB 22 KPVSLSRCCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81  
QY 61 YLEKALN 67  
DB 82 YLEKALN 88

#### RESULT 4

cytokine - mouse

C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I81182  
R:Tashiro, K.; Tada, H.; Heiker, R.; Shirazu, M.; Nakano, T.; Honjo, T.  
Science 261, 600-603, 1993  
A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I membr  
A:Reference number: I59582; MUID:93342488; PMID:8342023  
A:Accession: I81182  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-93 <RES>  
A:Cross-references: GB:L12030; NID:g393181; PIDN:AAA40101.1; PID:g393182  
C:Genetics:  
A:Gene: SDF-1-beta  
C:Superfamily: beta-thromboglobulin

Query Match 95.3%; Score 345; DB 2; Length 93;  
Best Local Similarity 95.5%; Pred. No. 6e-35;  
Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
DB 22 KPVSLSRCCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81

QY 61 YLEKALN 67  
DB 82 YLEKALN 88

#### RESULT 5

I48148  
Neutrophil attractant protein-1 - guinea pig

C:Species: Cavia porcellus (guinea pig)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Aug-1999  
C:Accession: I48148  
R:Yoshimura, T.; Johnson, D.G.  
J. Immunol. 151, 6225-6236, 1993  
A:Title: cDNA cloning and expression of guinea pig neutrophil attractant protein-1 (N  
A:Reference number: I48148; MUID:94065176; PMID:7504015  
A:Accession: I48148  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-101 <RES>  
A:Cross-references: GB:L04986; NID:g459764; PIDN:AAA37049.1; PID:g459765  
C:Genetics:  
A:Gene: NAP-1  
C:Superfamily: beta-thromboglobulin

Query Match 27.9%; Score 101; DB 2; Length 101;  
Best Local Similarity 35.9%; Pred. No. 4e-05;  
Matches 23; Conservative 16; Mismatches 17; Indels 8; Gaps 5;

QY 8 RCPCRFESHVARAN--VKHLKILNTPNCA-LQIVARLKNNNRQVCIDPKLKWIOEYL 62  
DB 33 RCQC--IKHTTPHFKFKELKVLIESGPCANSEIIVKL-SNROLCIDPKKMWQDVV 89

QY 63 EKAL 66  
DB 90 SMFL 93

#### RESULT 6

JN0841  
Interleukin-8 - dog

C:Species: Canis lupus familiaris (dog)  
C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 12-Apr-1995  
C:Accession: JN0841  
R:Ishikawa, J.; Suzuki, S.; Hotta, K.; Hirota, Y.; Mizuno, S.; Suzuki, K.  
Gene 131, 305-306, 1993  
A:Title: Cloning of a canine gene homologous to the human interleukin-8-encoding gene  
A:Reference number: JN0841; MUID:94010328; PMID:7916715  
A:Accession: JN0841  
A:Molecule type: DNA  
A:Residues: 1-95 <ISH>  
C:Comment: This protein is a polymorphonuclear leukocytes chemotactic factor and is i  
C:Genetics:  
A:Introns: 22/1: 67/2  
C:Superfamily: beta-thromboglobulin

Query Match 26.8%; Score 97; DB 2; Length 95;  
Best Local Similarity 34.8%; Pred. No. 0.00012;  
Matches 23; Conservative 15; Mismatches 20; Indels 8; Gaps 4;

QY 3 VSLPYRCPCRFESHVARANKHLKILNTPNCA-LQIVARLKNNNRQVCIDPKLKW 57  
DB 28 VSELRCQC--IKHTSTPHFKYIKELRVDSGPCENSEIIVKFNNGN-EVCLDPKEKW 84

QY 58 IOEYL 63  
DB 85 VQKVVQ 90



A:Molecule type: mRNA  
 A:Residues: 1-99 <RE2>  
 A:Cross-references: GB:M17017; NID:g179579; PIDN:AAA3611.1; PID:g179580  
 R:Kusner, D.J.; Luebers, E.L.; Nowinski, R.J.; Konieczkowski, M.; King, C.H.; Sedor, J.  
 Kidney Int. 39, 1240-1248, 1991  
 A:Title: Cytokine and LPS-induced synthesis of interleukin-8 from human mesangial cells  
 A:Reference number: 137902; MUID:91374977; PMID:1895676  
 A:Accession: 137902  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-97 <RE3>  
 A:Cross-references: EMBL:Z11686; NID:g333958; PIDN:CAA77745.1; PID:g333959  
 R:Alouani, S.; Gaertner, H.F.; Mermod, J.C.; Power, C.A.; Bacon, K.B.; Wells, T.N.C.; P.  
 Eur. J. Biochem. 227, 328-334, 1995  
 A:Title: A fluorescent interleukin-8 receptor probe produced by targeted labelling at t  
 A:Reference number: 567519; MUID:95154308; PMID:7851404  
 A:Accession: 567519  
 A:Molecule type: mRNA  
 A:Residues: 1-99 <ALO>  
 C:Comment: This secretory protein is chemotactic for polymorphonuclear leukocytes.  
 C:Comment: This protein is variably processed at the amino end. The major form differs i  
 C:Genetics:  
 A:Gene: GDB:118  
 A:Cross-references: GDB:120099; OMIM:146930  
 A:Map position: 4q13-4q21  
 A:Introns: 22/1; 67/2; 95/2  
 C:Superfamily: beta-chromoglobulin  
 C:Keywords: chemotaxis; cytokine; inflammation  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-99/Product: interleukin-8, minor form #status experimental <MATA>  
 F:23-99/Product: interleukin-8, major fibroblast-derived form #status experimental <MAT  
 F:28-99/Product: interleukin-8, major lymphocyte/monocyte-derived form #status experimen

Query Match 26.7%; Score 96.5; DB 2; Length 99;  
 Best Local Similarity 31.1%; Pred. No. 0.00014;  
 Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5;

QY 1 KGVSLP-----YRCPC-REFESHVARANVKHLKILNT-PNCA-LQIVARLKNRRQVCID 52  
 Db 21 EGAVLPSSAKELRCQCIKTYSKPRPKIKELRVIESGPHCANETIYKL-SDRELCLD 79

OY 53 PKLRWIDYLEKAL 66  
 Db 80 PKENWQVRVEKFL 93

RESULT 8  
 S42496  
 Interleukin-8 precursor [similarity] - sheep  
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 19-Jan-2001  
 R:Legasteleis, I.; Greenland, T.; Arnaud, P.; Mornex, J.F.; Cordier, G.  
 Submitted to the EMBL Data Library, March 1994  
 A:Description: Nucleotide sequence of ovine interleukin 8 cDNA using polymerase chain re  
 A:Reference number: S42496  
 A:Accession: S42496  
 A:Molecule type: mRNA  
 A:Residues: 1-101 <LEG>  
 A:Cross-references: EMBL:X78306; NID:g463253; PIDN:CAA55115.1; PID:g463254  
 R:Seow, H.F.; Yoshimura, T.; Wood, P.R.; Colditz, I.G.  
 Immunol. Cell Biol. 72, 398-405, 1994  
 A:Title: Cloning, sequencing, expression and inflammatory activity in skin of ovine inte  
 A:Reference number: I46997; MUID:95137691; PMID:7855964  
 A:Accession: I46997  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-101 <SEO>  
 A:Cross-references: GB:S74436; NID:g786590; PIDN:AAB3241.1; PID:g786591  
 C:Genetics:  
 A:Gene: IL-8  
 C:Superfamily: beta-thromboglobulin  
 C:Keywords: chemotaxis; cytokine; inflammation

F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-101/Product: interleukin-8 #status predicted <MAT>  
 Query Match 25.4%; Score 92; DB 2; Length 101;  
 Best Local Similarity 30.4%; Pred. No. 0.00051;  
 Matches 21; Conservative 20; Mismatches 20; Indels 8; Gaps 5;

QY 3 VSLPYRCPCREFESHVARAN---VKHLKILNT-PNCA-LQIVARLKNRRQVCIDPKLKW 57  
 Db 28 MSTELRCQC--IKTHSRPFHKFIKELRVIESGPHCENSEIYKL-TNGKEVCIDPREKM 84

OY 58 IQETLEKAL 66  
 Db 85 VQKVVQAF 93

RESULT 9  
 I48147  
 monocyte chemoattractant protein-1 - guinea pig  
 C:Species: Cavia porcellus (guinea pig)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
 R:Yoshimura, T.  
 J. Immunol. 150, 5025-5032, 1993  
 A:Title: cDNA cloning of guinea pig monocyte chemoattractant protein-1 and expression  
 A:Reference number: I48147; MUID:93267104; PMID:8496603  
 A:Accession: I48147  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-120 <RES>  
 A:Cross-references: GB:I04985; NID:g349820; PIDN:AAA37047.1; PID:g349821  
 C:Genetics:  
 A:Gene: MCP-1  
 C:Superfamily: macrophage inflammatory protein

Query Match 25.4%; Score 92; DB 2; Length 120;  
 Best Local Similarity 31.7%; Pred. No. 0.00061;  
 Matches 20; Conservative 11; Mismatches 30; Indels 2; Gaps 2;

QY 2 GVSILPYRCPCREFESHVARANVKHLKILNTPNCALQIVARLKNRRQVCIDPKLKWQEV 61  
 Db 27 GVNTP-TC-CYTFNKQIPLRKRVGERITSSRCQEAIVFRTLKKEVCADPTQKWQDY 84

OY 62 LEK 64  
 Db 85 IAK 87

RESULT 10  
 A32954  
 gro-alpha precursor - mouse  
 N:Alternate names: gro protein; growth regulated protein; melanoma growth-stimulating  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Oct-1989 #sequence\_revision 20-Oct-1989 #text\_change 20-Aug-1999  
 R:Ouendo, P.; Albertella, J.; Men, D.; Graycar, J.L.; Derynck, R.; Stiles, C.D.  
 J. Biol. Chem. 264, 4133-4137, 1989  
 A:Title: The platelet-derived growth factor-inducible KC gene encodes a secretory pro  
 A:Reference number: A32954; MUID:89139485; PMID:2917992  
 A:Accession: A32954  
 A:Molecule type: mRNA  
 A:Residues: 1-96 <OOU>  
 A:Cross-references: GB:J04596; NID:g201042; PIDN:AAA40131.1; PID:g201043  
 R:Riseck, R.P.; Macdonald-Bravo, H.; Mattei, M.G.; Bravo, R.  
 Exp. Cell Res. 180, 266-275, 1989  
 A:Title: Cloning and sequence of a secretory protein induced by growth factors in mou  
 A:Reference number: JH0081; MUID:89078502; PMID:2909392  
 A:Accession: JH0081  
 A:Molecule type: mRNA  
 A:Residues: 1-96 <RYS>  
 C:Comment: This protein is basic and lacks threonine, phenylalanine, and tyrosine.  
 C:Genetics:  
 A:Map position: 5









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OY 1 KVSFLPFCPCRFESHVARANVHKILNTPNCALQIVARLKNNNNOVCIDPKLKWIOE 60
DB 22 KPSVLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNNOVCIDPKLKWIOE 81
OY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 2
SDFL_HUMAN STANDARD: PRT: 93 AA.
AC P48061;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell
DE growth stimulating factor) (PBSE) (HIRH).
GN SDF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RA Spotila L.D.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=96039262; PubMed=7490086;
RA Shirozu M., Nakano T., Inazawa J., Tashiro K., Tada H.,
RA Shinohara T., Honjo T.;
RT "Structure and chromosomal localization of the human stromal cell-
RT derived factor 1 (SDF1) gene.";
RL Genomics 28:495-500(1995).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Liver;
RA Begun N.A., Barnard G.F.;
RT "Nucleotide sequence of hIRH, human Interline reduced in
RT hepatomas.";
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RN STRUCTURE BY NMR OF 22-88.
RX MEDLINE=98046030; PubMed=9384579;
RA Crump M.P., Gong J.H., Loetscher P., Rajaratnam K., Amara A.,
RA Arenzana-Seisdedos F., Virelizier J.L., Baggiolini M., Sykes B.D.,
RA Clark-Lewis I.;
RT "Solution structure and basis for functional activity of stromal
RT cell-derived factor-1, dissociation of CXCR4 activation from binding
RT and inhibition of HIV-1.";
RL EMBO J. 16:6996-7007(1997).
RN [5]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-88.
RX MEDLINE=98284037; PubMed=9618518;
RA Dealwis C., Fernandez E.J., Thompson D.A., Simon R.J., Siani M.A.,
RA Lolis E.;
RT "Crystal structure of chemically synthesized [N3A] stromal
RT cell-derived factor 1alpha, a potent ligand for the HIV-1 'fusin'
RT coreceptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:6941-6946(1998).
CC -1- FUNCTION: CHEMOATTRACTANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT
CC NOT NEUTROPHILS.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE);
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXK).
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CC -----
DR EMBL: U16752; AAA97434.1; -
DR EMBL: L36033; AAB39333.1; -
DR EMBL: L36034; AAB39333.1; -
DR EMBL: U19495; AAB40516.1; -
DR PDB: 1SDF; 28-JAN-98.
DR PDB: 2SDF; 17-JUN-98.
DR PDB: 1A15; 12-AUG-98.
DR Genew: HNCN:10672; SDF1.
DR MTM: 600835; -
DR InterPro: IPR001089; CXK_cimkine_sm1.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
KW Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing;
KW 3D-structure.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 93 STROMAL CELL-DERIVED FACTOR 1.
FT DISULFID 30 55
FT DISULFID 32 71
FT VARSPIC 90 93 MISSING (IN ISOFORM ALPHA).
SQ SEQUENCE 93 AA; 10666 MW; 505B5A29C2B44EBD CRC64;

Query Match 95.6%; Score 346; DB 1; Length 93;
Best Local Similarity 97.0%; Pred. No. 1; Ie-35;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KVSFLPFCPCRFESHVARANVHKILNTPNCALQIVARLKNNNNOVCIDPKLKWIOE 60
DB 22 KPSVLSYRCPCRFESHVARANVHKILNTPNCALQIVARLKNNNNOVCIDPKLKWIOE 81
OY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 3
SDFL_MOUSE STANDARD: PRT: 89 AA.
AC P40224;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell
DE growth stimulating factor) (PBSE) (12-O-tetradecanoylphorbol 13-
DE acetate repressed protein 1) (TPAR1) (Thymic lymphoma cell stimulating
DE factor) (TISF).
GN SDF1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=94181581; PubMed=8134392;
RA Nagasawa T., Kikutani H., Kishimoto T.;
RT "Molecular cloning and structure of a pre-B-cell growth-stimulating
RT factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:2305-2309(1994).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=93342488; PubMed=8342023;
RA Tashiro K., Tada H., Heikler R., Shirozu M., Nakano T., Honjo T.;
RT "Signal sequence trap: a cloning strategy for secreted proteins and
RT type I membrane proteins.";
RL Science 261:600-603(1993).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=95073497; PubMed=7982471;
RA Jiang W., Zhou P., Kahn S.M., Tomita N., Johnson M.D.,

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RA Weinstein I.B.:  
 RT "Molecular cloning of TPAP1, a gene whose expression is repressed by  
 the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA)."  
 RL Exp. Cell Res. 215:284-293(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-AKR/J;  
 RA Nomura M., Nakata Y., Uzuwa A., Nose M., Akashi M., Suzuki G.;  
 RL Submitted (DEC-1994) to the EMBL/Genbank/DDJJ databases.  
 CC -1- FUNCTION: CHEMOKINE-INDUCED ACTIVE ON T-LIMPHOCYTES, MONOCYTES, BUT  
 NOT NEUTROPHILS.  
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF BONE MARROW-DERIVED B  
 PRECURSOR CELLS IN THE PRESENCE OF IL-7 AS WELL AS GROWTH OF THE  
 CC ALTERNATIVE CELL-DEPENDENT B-CELL CLONE DM34 CELLS.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, ALPHA AND BETA (SHOWN HERE);  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: BELONGS TO THE INTERKINE ALPHA FAMILY (SMALL CYTOKINE  
 C-X-C) (CHEMOKINE CXC).  
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 CC -----  
 DR EMBL: D21072; BAA04648.1; -  
 DR EMBL: L12029; AAA40100.1; -  
 DR EMBL: L12030; AAA40101.1; -  
 DR EMBL: S74318; AAB32650.1; -  
 DR EMBL: D43804; BAA07862.1; -  
 DR EMBL: D43805; BAA07863.1; -  
 DR PIR: A53497; A53497.  
 DR HSSP: P48061; ISDF.  
 DR MGD: MGI:103556; Sdfl.  
 DR InterPro: IPR001089; CXC\_cmkline\_sml1.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PR00048; IL8; 1.  
 DR SMART: SM00199; SCY; 1.  
 DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; FALSE\_NEG.  
 DR Cytokine: Chemotaxis; Growth factor; Signal; Alternative splicing.  
 FT SIGNAL 1 19  
 FT CHAIN 20 89 STROMAL CELL-DERIVED FACTOR 1.  
 FT DISULFID 30 55  
 FT DISULFID 32 71 BY SIMILARITY.  
 FT VARSPLIC 89 89 K -> KRLKM (IN ISOFORM BETA).  
 SQ SEQUENCE 89 AA; 10032 MW; C4B8AD69078E55FA CRC64;  
 Query Match 95.3%; Score 345; DB 1; Length 89;  
 Best Local Similarity 95.5%; Pred. No. 1.4e-35;  
 Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 KGVSLPRCPREFESHVARANKHLILTPGALQIVARLKNNNROYCIDPKLWIOE 60  
 DB 22 KPVSLRCPREFESHVARANKHLILTPGALQIVARLKNNNROYCIDPKLWIOE 81  
 QY 61 YLEKALN 67  
 DB 82 YLEKALN 88  
 RESULT 4  
 ID IL8\_CANVO STANDARD; PRT; 101 AA.  
 AC P49113;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-8 precursor (IL-8) (CXCL8) (Neutrophil attractant protein  
 1) (NAP-1).  
 GN IL8  
 OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.  
 OC NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=94065176; PubMed=7504015;  
 RA Yoshimura T., Johnson D.G.;  
 RT "CDNA cloning and expression of guinea pig neutrophil attractant  
 protein-1 (NAP-1). NAP-1 is highly conserved in guinea pig."  
 RL J. Immunol. 151:6225-6236(1993).  
 CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,  
 BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN  
 CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN  
 CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE INTERKINE ALPHA FAMILY (SMALL CYTOKINE  
 C-X-C) (CHEMOKINE CXC).  
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 CC -----  
 DR EMBL: L04986; AAA37049.1; -  
 DR HSSP: P10145; 2IL8.  
 DR InterPro: IPR001089; CXC\_cmkline\_sml1.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PR00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTCKXC.  
 DR SMART: SM00199; SCY; 1.  
 DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; 1.  
 DR Cytokine: Chemotaxis; Inflammatory response; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 101 INTERLEUKIN-8.  
 FT DISULFID 34 61 BY SIMILARITY.  
 FT DISULFID 36 77 BY SIMILARITY.  
 SQ SEQUENCE 101 AA; 11414 MW; 557E2A9E15F6727F CRC64;  
 Query Match 27.9%; Score 101; DB 1; Length 101;  
 Best Local Similarity 35.9%; Pred. No. 1.3e-05;  
 Matches 23; Conservative 16; Mismatches 17; Indels 8; Gaps 5;  
 QY 8 RCPREFESHVARAN--VKHLKILNT-PNCA-LQIVARLKNNNROYCIDPKLWIOEYL 62  
 DB 33 RQCC--IKIHPPHFKPIKELKVIISGPCANSSEILVKL-SNRQCLCDPKKKWQDVY 89  
 QY 63 EKAL 66  
 DB 90 SMFL 93  
 RESULT 5  
 ID IL8\_CANFA STANDARD; PRT; 101 AA.  
 AC P41324;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-8 precursor (IL-8) (CXCL8).  
 GN IL8  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OC NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94010328; PubMed=7916715;  
 RA Ishikawa J., Suzuki S., Hotta K., Hirota Y., Mizuno S., Suzuki K.;  
 RT "Cloning of a canine gene homologous to the human

RT Interleukin-8-encoding gene.";  
 RL Gene 131:305-306(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph node;  
 RX MEDLINE=95127913; PubMed=7827282;  
 RA Matsumoto T., Mohamed A., Onodera T., Kato H., Ohashi T.,  
 RA Gotsuka R., Tsujimoto H., Hasegawa A., Furusawa S., Yoshinara K.,  
 RA Ishikawa J., Hotta K., Suzuki K., Hirota Y.;  
 RT "Molecular cloning and expression of canine Interleukin 8 cDNA.";  
 RL Cytokine 6:455-461(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Mongrel; TISSUE=Jugular vein;  
 RX MEDLINE=95114148; PubMed=7814650;  
 RA Kikela G.L., Smith W.C., Larosa G.J., Manning A.M.,  
 RA Mendoza L.H., Daly T.J., Hughes B.J., Youker K.A., Hawkins H.K.,  
 RA Michael L.H., Rot A., Entman M.L.;  
 RT "Interleukin-8 gene induction in the myocardium after ischemia and  
 RT reperfusion in vivo.";  
 RL J. Clin. Invest. 95:89-103(1995).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Beagle;  
 RX MEDLINE=97230298; PubMed=9119462;  
 RA Straubinger R.K., Straubinger A.F., Harter L., Jacobson R.H.,  
 RA Chang Y.-F., Summers B.A., Erb H.N., Appel M.J.;  
 RT "Morrelia burgdorferi migrates into joint capsules and causes an up-  
 RT regulation of interleukin-8 in synovial membranes of dogs  
 RT experimentally infected with ticks.";  
 RL Infect. Immun. 65:1273-1285(1997).  
 CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,  
 CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN  
 CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN  
 CC RESPONSE TO AN INFLAMMATORY STIMULUS.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE  
 CC C-X-C) (CHEMOKINE CX-C).  
 CC -----  
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 CC -----  
 DR EMBL: D28772; BAA05961.1; -;  
 DR EMBL: D14285; BAA03246.1; -;  
 DR EMBL: U10308; AAC48434.1; -;  
 DR EMBL: AF048717; AAC05134.1; -;  
 DR HSSP: P10145; 1IKM.  
 DR InterPro: IPR001089; CX-C\_chim\_kine\_sm1.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTKCXC.  
 DR SMART: SM00199; SCY; 1.  
 DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; 1.  
 KW Cytokine; Chemotaxis; Inflammatory response; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 101  
 FT DISULFID 34 61  
 FT DISULFID 36 77  
 FT DISULFID 36 77  
 SQ SEQUENCE 101 AA; 11280 MW; 3A3A4676DA968376 CRC64;  
 Query Match 27.6%; Score 100; DB 1; Length 101;  
 Best Local Similarity 36.1%; Pred. No. 1.7e-05;  
 Matches 26; Conservative 15; Mismatches 19; Indels 12; Gaps 5;  
 QY 3 VSUPLYRCPCRFESHVAVANKHLKILNT---PNCALQIVARLKNNNOVCIDPLTKW 57  
 DB 28 VSSELRCQC--IKTHSPFPFKYIKELRVIDSQPHCENSEITVAVLNGN-EVCDPKRKW 84

OY 58 IOE----YLEKA 65  
 DB 85 VOKVQIFLKKA 96  
 RESULT 6  
 ID IL8\_FELCA STANDARD; PRT; 101 AA.  
 AC OQXSX5;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-8 precursor (IL-8) (CXCL8).  
 GN IL8.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Straubinger A.F., Simpson K.W., Straubinger R.K.;  
 RT "Feline interleukin-8 mRNA.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,  
 CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN  
 CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN  
 CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE  
 CC C-X-C) (CHEMOKINE CX-C).  
 CC -----  
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 CC -----  
 DR EMBL: AF158598; AAD40323.1; -;  
 DR HSSP: P10145; 1IKM.  
 DR InterPro: IPR001089; CX-C\_chim\_kine\_sm1.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTKCXC.  
 DR SMART: SM00199; SCY; 1.  
 DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; 1.  
 KW Cytokine; Chemotaxis; Inflammatory response; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 101  
 FT DISULFID 34 61  
 FT DISULFID 36 77  
 FT DISULFID 36 77  
 SQ SEQUENCE 101 AA; 11165 MW; 690D97F13EF79170 CRC64;  
 Query Match 26.8%; Score 97; DB 1; Length 101;  
 Best Local Similarity 33.3%; Pred. No. 4.1e-05;  
 Matches 22; Conservative 18; Mismatches 18; Indels 8; Gaps 5;  
 QY 3 VSUPLYRCPCRFESHVAVAN---VKHLKILNT-PNCALQIVARLKNNNOVCIDPLTKW 57  
 DB 28 ISSELRCQC--IKTHSPFPFKYIKELRVIDSQPHCENSEITVAVLNGKEVCIDPKRW 84  
 OY 58 IOEYLE 63  
 DB 85 VQKVE 90  
 RESULT 7  
 ID IL8\_HUMAN STANDARD; PRT; 99 AA.  
 AC P10145; O9C077; O96RG6;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-8 precursor (IL-8) (CXCL8) (Monocyte-derived neutrophil  
 DE chemotactic factor) (MDC8) (T-cell chemotactic factor) (Neutrophil-  
 DE activating protein 1) (NAP-1) (Lymphocyte-derived neutrophil-  
 DE activating factor) (LYNAP) (Protein 3-10C) (Neutrophil-activating  
 DE factor) (NAF) (Granulocyte chemotactic protein 1) (GCP-1) (Emoctakin).  
 GN IL8.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88258376; PubMed=3260265;  
 RA Matsushima K., Morishita K., Yoshimura T., Lavi S., Kobayashi Y.,  
 RA Lew W., Appella E., Kung H., Leonard E.J., Oppenheim J.J.;  
 RT "Molecular cloning of a human monocyte-derived neutrophil chemotactic  
 RT factor (MDC8) and the induction of MDC8 mRNA by Interleukin 1 and  
 RT tumor necrosis factor.";  
 RL J. Exp. Med. 167:1883-1893(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87224164; PubMed=2953813;  
 RA Schmid J., Weissmann C.;  
 RT "Induction of mRNA for a serine protease and a  
 RT beta-thromboglobulin-like protein in mitogen-stimulated human  
 RT leukocytes.";  
 RL J. Immunol. 139:250-256(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89313739; PubMed=2664463;  
 RA Kowalski J., Denhardt D.T.;  
 RT "Regulation of the mRNA for monocyte-derived neutrophil-activating  
 RT peptide in differentiating HL60 promyelocytes.";  
 RL Mol. Cell. Biol. 9:1946-1957(1989).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89309826; PubMed=2663993;  
 RA Mukaida N., Shitoo M., Matsushima K.;  
 RT "Genomic structure of the human monocyte-derived neutrophil  
 RT chemotactic factor IL-8.";  
 RL J. Immunol. 143:1366-1371(1989).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Ishikawa J.;  
 RT Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RA Jang J.S., Kim B.E.;  
 RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
 RA Nickerson D.A.;  
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP SEQUENCE OF 23-46.  
 RX MEDLINE=89246368; PubMed=2655583;  
 RA Golds E.E., Mason P., Nyirkos P.;  
 RT "Inflammatory cytokines induce synthesis and secretion of gro protein  
 RT and a neutrophil chemotactic factor but not beta 2-microglobulin in  
 RT human synovial cells and fibroblasts.";  
 RL Biochem. J. 259:585-588(1989).  
 RN [9]  
 RP SEQUENCE OF 23-54.  
 RX MEDLINE=89279141; PubMed=2659722;  
 RA Suzuki K., Miyasaka H., Ota H., Yamakawa Y., Tagawa M., Kuramoto A.,  
 RA Mizuno S.;  
 RT "Purification and partial primary sequence of a chemotactic protein  
 RT for polymorphonuclear leukocytes derived from human lung giant cell  
 RT carcinoma L055C cells.";  
 RL J. Exp. Med. 169:1895-1901(1989).  
 RN [10]

RP SEQUENCE OF 28-99.  
 RX MEDLINE=88162914; PubMed=3279957;  
 RA Gregory H., Young J., Schroeder J.M., Mrowietz U., Christophers E.;  
 RT "Structure determination of a human lymphocyte derived neutrophil  
 RT activating peptide (LYNAP).";  
 RL Biochem. Biophys. Res. Commun. 151:883-890(1988).  
 RN [11]  
 RP SEQUENCE OF 28-59.  
 RX MEDLINE=88106502; PubMed=3322281;  
 RA Walz A., Feveri P., Aschauer H., Baggiolini M.;  
 RT "Purification and amino acid sequencing of NAF, a novel neutrophil-  
 RT activating factor produced by monocytes.";  
 RL Biochem. Biophys. Res. Commun. 149:755-761(1987).  
 RN [12]  
 RP SEQUENCE OF 28-69.  
 RX MEDLINE=88097462; PubMed=3480540;  
 RA Yoshimura T., Matsushima K., Tanaka S., Robinson E.A., Appella E.,  
 RA Oppenheim J.J., Leonard E.J.;  
 RT "Purification of a human monocyte-derived neutrophil chemotactic  
 RT factor that has peptide sequence similarity to other host defense  
 RT cytokines.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:9233-9237(1987).  
 RN [13]  
 RP N-TERMINAL FORMS.  
 RX MEDLINE=91006326; PubMed=2145175;  
 RA van Damme J., Rampart M., Conling R., Decock B., van Osselaer N.,  
 RA Willems J., Billiau A.;  
 RT "The neutrophil-activating proteins interleukin 8 and beta-  
 RT thromboglobulin: in vitro and in vivo comparison of NH2-terminally  
 RT processed forms.";  
 RL Eur. J. Immunol. 20:2113-2118(1990).  
 RN [14]  
 RP N-TERMINAL FORMS.  
 RX MEDLINE=89233715; PubMed=2523801;  
 RA van Damme J., van Beeumen J., Conings R., Decock B., Billiau A.;  
 RT "Purification of granulocyte chemotactic peptide/interleukin-8  
 RT reveals N-terminal sequence heterogeneity similar to that of  
 RT beta-thromboglobulin.";  
 RL Eur. J. Biochem. 181:337-344(1989).  
 RN [15]  
 RP SYNTHESIS OF 28-99.  
 RX MEDLINE=9115767; PubMed=2007144;  
 RA Clark-Lewis I., Mose B., Walz A., Baggiolini M., Scott G.J.,  
 RA Aebersold R.;  
 RT "Chemical synthesis, purification, and characterization of two  
 RT inflammatory proteins, neutrophil activating peptide 1  
 RT (interleukin-8) and neutrophil activating peptide.";  
 RL Biochemistry 30:3128-3135(1991).  
 RN [16]  
 RP REVIEW.  
 RX MEDLINE=92347562; PubMed=1639201;  
 RA Baggiolini M., Clark-Lewis I.;  
 RT "Interleukin-8, a chemotactic and inflammatory cytokine.";  
 RL FEBS Lett. 307:97-101(1992).  
 RN [17]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=90234679; PubMed=2184886;  
 RA Clore G.M., Appella E., Yamada M., Matsushima K., Gronenborn A.M.;  
 RT "Three-dimensional structure of Interleukin 8 in solution.";  
 RL Biochemistry 29:1689-1696(1990).  
 RN [18]  
 RP STRUCTURE BY NMR OF COMPLEX TO RECEPTOR.  
 RX MEDLINE=99148123; PubMed=10368283;  
 RA Skelton N.J., Quan C., Reilly D., Lowman H.;  
 RT "Structure of a CXCL chemokine-receptor fragment in complex with  
 RT interleukin-8.";  
 RL Structure 7:157-168(1999).  
 RN [19]  
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 RX MEDLINE=90216714; PubMed=2182630;  
 RA Baldwin E.T., Franklin K.A., Appella E., Yamada M., Matsushima K.,  
 RA Wlodawer A., Weber I.T.;  
 RT "Crystallization of human Interleukin-8. A protein chemotactic for

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RT neutrophils and T-lymphocytes."
RL J. Biol. Chem. 265:6851-6853(1990).
RN [20]
RP X-RAY CRYSTALLOGRAPHY, AND STRUCTURE BY NMR.
RA MEDLINE=91171286; PubMed=2005614;
RX Clore G.M., Gronenborn A.M.;
RT "Comparison of the solution nuclear magnetic resonance and crystal
RT structures of interleukin-8. Possible implications for the mechanism
RT of receptor binding."
RL J. Mol. Biol. 217:611-620(1991).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS), AND STRUCTURE BY NMR.
RX MEDLINE=91110556; PubMed=1988949;
RA Baldwin E.T., Weber I.T., St Charles R., Xuan J.C., Appella E.,
RA Yamada M., Matsushima K., Edwards B.F., Clore G.M., Gronenborn A.M.;
RT "Crystal structure of interleukin 8: symbiosis of NMR and
RT crystallography."
RL Proc. Natl. Acad. Sci. U.S.A. 88:502-506(1991).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF MUTANT.
RX MEDLINE=20178334; PubMed=10707023;
RA Gebler N., Lowman H., Artis D.R., Eigenbrodt C.;
RT "Receptor-binding conformation of the 'ELR' motif of IL-8: X-ray
RT structure of the USC/H33C variant at 2.35 A resolution."
RL Protein 38:361-367(2000).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXK).
CC -----
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CC -----
DR EMBL: Y00787; CAA68742.1; -
DR EMBL: M17017; AAA35611.1; -
DR EMBL: M26383; AAA36323.1; -
DR EMBL: M28130; AAA59158.1; -
DR EMBL: D14283; BAA03245.1; -
DR EMBL: AF043337; AAK00048.1; -
DR EMBL: AF385626; AAK60276.1; ALT_SEQ.
DR PIR: A37034; A37034.
DR PIR: S03975; S03975.

Query Match 26.7%; Score 96.5; DB 1; Length 99;
Best Local Similarity 31.1%; Pred. No. 4.6e-05;
Matches 23; Conservative 19; Mismatches 23; Indels 9; Gaps 5;

OY 1 KGVSLP-----YRCP-REFESHVARANKHLKILNT-PNCA-LQIVARLKNRRVOCID 52
DB 21 EGAVLPRSAKELRCQCIKTKYKSPFHPKFIKELNVIESGPHCANTETIIVKL-SDGRELCLD 79
OY 53 PKLKWIOEYLEKAL 66
DB 80 PKEPWQVRVEKFL 93

RESULT 8
ID IL8_MACMU STANDARD; PRT; 101 AA.
AC P51495;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN IL8.

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OS Macaca mulatta (Rhesus macaque), and
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Bar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates."
RL J. Immunol. 155:3946-3954(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Macaca mulatta; TISSUE=Blood;
RX MEDLINE=95355132; PubMed=762861;
RA Minnerly J.C., Baganoif M.P., Deppeler C.L., Keller B.T.,
RA Rapp S.R., Wlodewski D.L., Fretland D.J., Bolanowski M.A.;
RT "Identification and characterization of rhesus macaque
RT interleukin-8."
RL Inflammation 19:313-331(1995).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXK).
CC -----
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CC -----
DR EMBL: U19849; AAA86711.1; -
DR EMBL: U19851; AAA86713.1; -
DR EMBL: S78555; AAA80141.2; -
DR HSSP: P10145; 2IL8.
DR InterPro: IPR001089; CXK_cmkine_sm1.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTKCXK.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Chemotaxis; Inflammatory response; Signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 101 INTERLEUKIN-8.
FT DISULFID 34 61 BY SIMILARITY.
FT DISULFID 36 77 BY SIMILARITY.
SQ SEQUENCE 101 AA; 11320 MW; 42BCF9C97C84B5F9 CRC64;

Query Match 25.8%; Score 93.5; DB 1; Length 101;
Best Local Similarity 30.6%; Pred. No. 0.00011;
Matches 22; Conservative 19; Mismatches 22; Indels 9; Gaps 5;

OY 1 KGVSLP-----YRCP-REFESHVARANKHLKILNT-PNCA-LQIVARLKNRRVOCID 52
DB 21 EGAVLPRSAKELRCQCIKTKYKSPFHPKFIKELNVIESGPHCANTETIIVKL-SDGRELCLD 79
OY 53 PKLKWIOEYLEK 64
DB 80 PKEPWQVRVEK 91

RESULT 9
ID IL8-SHEEP STANDARD; PRT; 101 AA.
AC P36925;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN IL8.

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DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
CN IL8.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95121931; PubMed=7821808;
RA Legesteels I., Greenland T., Arnaud P., Mornex J.F., Cordier G.;
RT "Sequencing of the ovine Interleukin-8-encoding cDNA using the
RT polymerase chain reaction.";
RL Gene 150:367-369(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95137691; PubMed=7835984;
RA Seow H.F., Yoshimura T., Wood P.R., Colditz I.G.;
RT "Cloning, sequencing, expression and inflammatory activity in skin of
RT ovine Interleukin-8.";
RL Immunol. Cell Biol. 72:398-405(1994).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS. BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
-----
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CC EMBL: X78306; CAAS5115.1; -
DR EMBL: S74436; AAB33241.1; -
DR PIR: S42496; S42496.
DR HSSP: P10145; 1IKM.
DR InterPro: IPR001089; CXC_chemkine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00437; SMALLCYTCKXC.
DR PRINTS: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Chemotaxis; Inflammatory response; Signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 101 INTERLEUKIN-8.
FT DISULFID 34 61 BY SIMILARITY.
FT DISULFID 36 77 BY SIMILARITY.
SO SEQUENCE 101 AA: 11292 MW: 40E8418B57C56A5B CRC64;

Query Match 25.4%; Score 92; DB 1; Length 101;
Best Local Similarity 30.4%; Pred. No. 0.00017;
Matches 21; Conservative 20; Mismatches 20; Indels 8; Gaps 5;
OY 3 VSLPYRCPCRFESVAVRAN--VKHLKILNT-PCNCA-LOIYARLKNNNROYCIDPKLKW 57
DB 28 MTELRRCOC-1KTHSTPHPKFKELRYIESGPHENSEITVKL-TNCKEVLDPKRW 84
OY 58 IOEYLEKAL 66
DB 85 VQKVQAF 93

RESULT 10
SY02_CAVPO STANDARD; PRT; 120 AA.
ID SY02_CAVPO

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AC Q08782;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
CN SCYA2 OR MCP1.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Z; TISSUE=Spleen;
RX MEDLINE=93267104; PubMed=8496603;
RA Yoshimura T.;
RT "cDNA cloning of guinea pig monocyte chemoattractant protein-1 and
RT expression of the recombinant protein.";
RL J. Immunol. 150:5025-5032(1993).
CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES, BUT NOT
CC NEUTROPHILS.
CC -1- SUBUNIT: MONOMER OR HOMODIMER. IN EQUILIBRIUM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
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CC EMBL: L04985; AAA37047.1; -
DR HSSP: P80098; 1B00.
DR InterPro: IPR000827; CC_chemkine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; Signal; Inflammatory response; Glycoprotein.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 120 SMALL INDUCIBLE CYTOKINE A2.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT DISULFID 33 57 SIMILARITY).
FT DISULFID 34 73 BY SIMILARITY.
FT CARBOHYD 97 97 N-LINKED (GLUCNA... ) (POTENTIAL).
SO SEQUENCE 120 AA: 13741 MW: 5905596851CFF1C54 CRC64;

Query Match 25.4%; Score 92; DB 1; Length 120;
Best Local Similarity 31.7%; Pred. No. 0.0002;
Matches 20; Conservative 11; Mismatches 30; Indels 2; Gaps 2;
OY 2 GVSLEPRCPCRFESVAVRANKHLKILNTPNCAQIYARLKNNNROYCIDPKLKIORY 61
DB 27 GVNTP-TC-CYFNKQIPLKRVKGYERTISSRCPOEAVIFRLKNEVCADPTQKWQDY 84
OY 62 LEK 64
DB 85 TAK 87

RESULT 11
GRO_MOUSE
ID GRO_MOUSE STANDARD; PRT; 96 AA.
AC P12850;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Growth regulated protein precursor (CXCL1) (Platelet-derived growth
DE factor-inducible protein KC) (Secretory protein NS1).

```

GN SCYB1 OR GRO1 OR GRO OR MGSA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89139485; PubMed=2917992;  
 RA Oquendo P., Alberta J., Wen D., Graycar J.L., Derynck R., Stiles C.D.;  
 RT "The platelet-derived growth factor-inducible KC gene encodes a  
 RT secretory protein related to platelet alpha-granule proteins.";  
 RL J. Biol. Chem. 264:4133-4137(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89078502; PubMed=2909392;  
 RA Ryseck R.P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;  
 RT "Cloning and sequence of a secretory protein induced by growth  
 RT factors in mouse fibroblasts.";  
 RL Exp. Cell Res. 180:266-275(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/Sv;  
 RA Bozic C.R., Kolakowski L.F. Jr., von Uexkull C., Garcia-Rodriguez M.,  
 RA Conklyn M.J., Breslow R., Showell H.J., Gerard N.P., Gerard C.;  
 RL Submitted (FEB-1995) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-10 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=96016008; PubMed=7561058;  
 RA Ohmori Y., Fukumoto S., Hamilton T.A.;  
 RT "Two structurally distinct kappa B sequence motifs cooperatively  
 RT control LPS-induced KC gene transcription in mouse macrophages.";  
 RL J. Immunol. 155:3593-3600(1995).  
 CC -1- FUNCTION: HAS CHEMOKINE ACTIVITY FOR NEUTROPHILS CONTRIBUTES TO  
 CC NEUTROPHIL ACTIVATION DURING INFLAMMATION (BY SIMILARITY).  
 CC -1- INDUCTION: BY PLATELET-DERIVED GROWTH FACTOR, IN LUNG, BY  
 CC LIPOPOLYSACCHARIDE OR INFLAMMATION (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE  
 CC C-X-C) (CHEMOKINE CXK).  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: J04596; AAA40131.1; -;  
 DR EMBL: U20634; AAB03376.1; -;  
 DR EMBL: U20527; AAB03376.1; JOINED.  
 DR EMBL: S79767; -; NOT\_ANNOTATED\_CDS.  
 DR PIR: A32954; A32954.  
 DR PIR: JH0081; JH0081.  
 DR HSSP: P19875; IONK.  
 DR MGD: MGI:108068; Gro1.  
 DR InterPro: IPR001089; CXK\_chkline\_smll.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTKCX.  
 DR SMART: SM00199; SCY; 1.  
 DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; 1.  
 KW Cytokine; Growth factor; Inflammatory response; Signal.  
 FT SIGNAL 1 24 PROBABLE.  
 FT CHAIN 25 96 GROWTH REGULATED PROTEIN.  
 FT DISULFID 33 59 BY SIMILARITY.  
 FT DISULFID 35 75 BY SIMILARITY.  
 SQ SEQUENCE 96 AA: 10254 MW: 4A52B5EC38B45C2 CRC64;

Query Match 25.3%; Score 91.5; DB 1; Length 96;  
 Best Local Similarity 32.8%; Pred. No. 0.00018;  
 Matches 20; Conservative 17; Mismatches 21; Indels 3; Gaps 3;

OY 8 RCPREFESHVARNYKHLKIL-NTPNCA-LQIVARKNNROVCLDPKIKIQEYLEKA 65  
 DB 32 RCQCLTFMAGIHILKNIQSLKVLPSGPHCTQTEVIATLK-NGRACIDPEAPLVQKIVQKM 90  
 OY 66 L 66  
 DB 91 L 91  
 RESULT 12  
 SY05\_MOUSE  
 ID SY05\_MOUSE STANDARD; PRT; 91 AA.  
 AC P30882;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES  
 DE protein) (SIS-delta) (Murantes).  
 GN SCYA5.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92277990; PubMed=1375672;  
 RA Heeger P., Wolf G., Meyers C., Sun M.J., O'Farrell S.C.,  
 RA Krensky A.M., Nelson E.G.;  
 RT "Isolation and characterization of cDNA from renal tubular epithelium  
 RT encoding murine Rantes.";  
 RL Kidney Int. 41:220-225(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92289805; PubMed=1376260;  
 RA Schall T.J., Simpson N.J., Mak J.Y.;  
 RT "Molecular cloning and expression of the murine RANTES cytokine:  
 RT structural and functional conservation between mouse and man.";  
 RL Eur. J. Immunol. 22:1477-1481(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NIH Swiss;  
 RX MEDLINE=94132613; PubMed=7507961;  
 RA Danoff T.M., Lalley P.A., Chang Y.S., Heeger P.S., Neilson E.G.;  
 RT "Cloning, genomic organization, and chromosomal localization of the  
 RT scya5 gene encoding the murine chemokine RANTES.";  
 RL J. Immunol. 152:1182-1189(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RX MEDLINE=94217689; PubMed=7513046;  
 RA Shin H.S., Drysdale B.E., Shin M.L., Noble P.W., Fisher S.N.,  
 RA Pazneke W.A.;  
 RT "Definition of a lipopolysaccharide-responsive element in the 5'-  
 RT flanking regions of Murantes and crg-2.";  
 RL Mol. Cell. Biol. 14:2914-2925(1994).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/CJ, B10.S/J, MOD/LTY, and SJL/J; TISSUE=Spleen;  
 RA R.Z., Teuscher C.;  
 RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER  
 CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM  
 CC BASOPHILS AND ACTIVATES EOSINOPHILS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: T-CELL AND MACROPHAGE SPECIFIC.  
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE  
 CC C-C) (CHEMOKINE CC).  
 CC -----  
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DR EMBL: M77747: AAA40029.1: -

DR EMBL: S37648: AAB22302.1: -

DR EMBL: U02298: AAB18302.1: -

DR EMBL: X70675: CA550011.1: -

DR EMBL: AF065944: AAC17511.1: -

DR EMBL: AF065945: AAC17512.1: -

DR EMBL: AF065946: AAC17513.1: -

DR EMBL: AF065947: AAC17514.1: -

DR HSSP: P13501: IRTN.

DR MCD: MGI:98262: SCYA5.

DR InterPro: IPR000827: CC\_chemkine\_sml.

DR InterPro: IPR001811: Chemokine\_IL8.

DR Pfam: PF00048: IL8: 1.

DR SMART: SM00199: SCY: 1.

DR PROSITE: PS00472: SMALL\_CYTOKINES\_CC: 1.

KW Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5.

FT DISULFID 33 57 BY SIMILARITY.

FT DISULFID 34 73 BY SIMILARITY.

FT CONFLICT 19 19 T -> A (IN REF. 2).

FT CONFLICT 41 41 A -> E (IN REF. 1).

SO SEQUENCE 91 AA: 10071 MW: 5DFD66F4684FE1C8 CRC64:

Query Match 25.1% Score 91: DB 1: Length 91:  
Best Local Similarity 37.1% Pred. No. 0.0002;  
Matches 23: Conservative 9: Mismatches 24: Indels 6: Gaps 3:

OY 6 PY---RCPCREFESHVA--RANVKHLKILTPNCALQIVARLKNNNROVCDIPKIKWIOE 60  
|| || | : | ||: || : | : | |||| | : ||: ||  
DB 25 PYGSDTTPCCFAYLSIALPRAHKEY-FYTSSKSNLAVVYTRRNOVCANPEKKWOE 83

OY 61 YL 62  
|:  
DB 84 YL 85

RESULT 13  
SY05\_RAT STANDARD: PRT: 92 AA.

AC P50231:  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Small inducible cytokine A5 precursor (CCL5) ('T-cell specific RANTES protein) (SIS-delta).  
GN SCYA5.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Long Evans; TISSUE=Lung;  
RA Jones M.L., Shanley T.P., Ward P.A.;  
RL Submitted (Feb-1994) to the EMBL/Genbank/DBJ databases.  
CC -1- FUNCTION: CHEMOTACTIC FOR BLOOD MONOCYTES, MEMORY T HELPER  
CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM  
CC BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE  
CC C-C) (CHEMOKINE CC).

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CC EMBL: U06436: AAA96499.1: -

DR HSSP: P13501: IRTN.

DR InterPro: IPR000827: CC\_chemkine\_sml.

DR InterPro: IPR001811: Chemokine\_IL8.

DR Pfam: PF00048: IL8: 1.

DR SMART: SM00199: SCY: 1.

DR PROSITE: PS00472: SMALL\_CYTOKINES\_CC: 1.

KW Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.

FT SIGNAL 1 24 POTENTIAL.

FT CHAIN 25 92 SMALL INDUCIBLE CYTOKINE A5.

FT DISULFID 34 58 BY SIMILARITY.

FT DISULFID 35 74 BY SIMILARITY.

SO SEQUENCE 92 AA: 10170 MW: B4FECC2B4208AC6 CRC64:

Query Match 25.1% Score 91: DB 1: Length 92:  
Best Local Similarity 37.1% Pred. No. 0.0002;  
Matches 23: Conservative 9: Mismatches 24: Indels 6: Gaps 3:

OY 6 PY---RCPCREFESHVA--RANVKHLKILTPNCALQIVARLKNNNROVCDIPKIKWIOE 60  
|| || | : | ||: || : | : | |||| | : ||: ||  
DB 26 PYGSDTTPCCFAYLSIALPRAHKEY-FYTSSKSNLAVVYTRRNOVCANPEKKWOE 84

OY 61 YL 62  
|:  
DB 85 YL 86

RESULT 14  
IL8\_PIG STANDARD: PRT: 103 AA.

AC P26894: P22951:  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Interleukin-8 precursor (IL-8) (CXCL8) (Alveolar macrophage chemotactic factor 1) (AMCF-1).  
GN IL8.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94103307; PubMed=8276881;  
RA Lin G., Pearson A.E., Scamurra R.W., Zhou Y., Baarsch M.J.,  
RA Weiss D.J., Murtough M.P.;  
RT "Regulation of Interleukin-8 expression in porcine alveolar  
RT macrophages by bacterial lipopolysaccharide.";  
RL J. Biol. Chem. 269:77-85(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Sanjanwala M.;  
RL Submitted (JUL-1991) to the EMBL/Genbank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 26-45.  
RC TISSUE=Lung;  
RX MEDLINE=93041741; PubMed=1420165;  
RA Goodman R.B., Foster D.C., Mathewes S.L., Osborn S.G., Kuljper J.L.,  
RA Forstrom J.W., Martin T.R.;  
RT "Molecular cloning of porcine alveolar macrophage-derived neutrophil  
RT chemotactic factors I and II: identification of porcine IL-8 and  
RT another interleukin-alpha protein.";  
RL Biochemistry 31:10483-10490(1992).  
RN [4]  
RP REVISION TO 23.  
RA Goodman R.B.;  
RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 26-45.  
RC STRAIN=Yorkshire;  
RX MEDLINE=91217086; PubMed=1850745;  
RA Goodman R.B., Forstrom J.W., Osborn S.G., Chl E.Y., Martin T.R.;

```

RT "Identification of two neutrophil chemotactic peptides produced by
RT porcine alveolar macrophages."
RL J. Biol. Chem. 266:8455-8463(1991).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- TISSUE SPECIFICITY: ALVEOLAR MACROPHAGES.
CC -1- INDUCTION: BY LIPOLYSACCHARIDE (LPS).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXCL).
CC -----
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CC -----
DR EMBL: M86923; AAA16616.1; -
DR EMBL: X61151; CAA43461.1; -
DR EMBL: M99367; AAA92576.1; -
DR PIR: A44253; A44253.
DR PIR: A39819; A39819.
DR HSSP: P10145; 11KM.
DR InterPro: IPR001089; CXCL_chemokine_sm1.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PRO0437; SMALLCYTKCX.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
DR Cytokine: Chemotaxis; Inflammatory response; Signal.
KW SIGNAL; 1; 25
FT CHAIN 26 103 INTERLEUKIN-8.
FT DISULFID 34 61 BY SIMILARITY.
FT DISULFID 36 77 BY SIMILARITY.
FT CONFLICT 33 34 RC -> CR (IN REF. 5).
FT CONFLICT 87 87 K -> KK (IN REF. 2).
SQ SEQUENCE 103 AA: 11633 MW: 9FE0E350E1928C64 CRC64;

Query Match 25.1%; Score 91; DB 1; Length 103;
Best Local Similarity 31.8%; Pred. No. 0.00023;
Matches 21; Conservative 18; Mismatches 19; Indels 8; Gaps 5;

QY 3 VSLPRCPGCFEFESHVARN---VKHLKIILNT-PNCA-LOIVARLNNNOVCIDPRKLW 57
DB 28 VSAELRCQC--INTHSTPFHPKFKELRVIESGPHCENSEIIVKLV-NGREVCIDPREKW 84
QY 58 IOEYLE 63
DB 85 VQKVVQ 90

RESULT 15
IL8 CERTO STANDARD: PRT: 101 AA.
AC P46653;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN IL8
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBL_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;

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```

RA Villinger F.J., Brar S.S., Wayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates."
RL J. Immunol. 155:3946-3954(1995).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXCL).
CC -----
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CC -----
DR EMBL: U19839; AAA86705.1; -
DR HSSP: P10145; 21L8.
DR InterPro: IPR001089; CXCL_chemokine_sm1.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PRO0437; SMALLCYTKCX.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
DR Cytokine: Chemotaxis; Inflammatory response; Signal.
KW SIGNAL; 1; 22
FT CHAIN 23 101 INTERLEUKIN-8.
FT DISULFID 34 61 BY SIMILARITY.
FT DISULFID 36 77 BY SIMILARITY.
SQ SEQUENCE 101 AA: DE14CEB4BC089D7 CRC64;

Query Match 24.7%; Score 89.5; DB 1; Length 101;
Best Local Similarity 29.7%; Pred. No. 0.00034;
Matches 22; Conservative 19; Mismatches 24; Indels 9; Gaps 5;

QY 1 KGVSILP-----YRCPC-RFEESHVARNYKHLKIILNT-PNCA-LOIVARLNNNOVCID 52
DB 21 EGAVLPSSAKELRCICIKYTSKPFHPKFKELRVIESGPHCVTEIIVKL-SDGRELCID 79
QY 53 PKLKIOWEYLEKAL 66
DB 80 KPEPWQGVVERKFL 93

```

Search completed: January 23, 2003, 15:34:19  
Job time : 7 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 23, 2003, 15:30:38 : Search time 22.6 Seconds  
(without alignments)  
610.848 Million cell updates/sec

Title: US-09-852-424-3  
Perfect score: 362  
Sequence: 1 KGVSLPYRCPREFSHVAR.....QVCIDPKLKIWELEKALN 67

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP-archaea:\*  
2: SP-bacteria:\*  
3: SP-fungi:\*  
4: SP-human:\*  
5: SP\_invertebrate:\*  
6: SP\_mammal:\*  
7: SP\_mhc:\*  
8: SP-organella:\*  
9: SP-phage:\*  
10: SP-plant:\*  
11: SP-rodent:\*  
12: SP\_virus:\*  
13: SP\_vertebrate:\*  
14: SP\_unclassified:\*  
15: SP\_virus:\*  
16: SP\_bacteriophage:\*  
17: SP\_archaeal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	346	95.6	92	4 Q9H554	Q9H554 homo sapien
2	338	93.4	89	11 Q90ZD1	Q90ZD1 ratius norv
3	285	78.7	94	13 Q8U0U9	Q8U0U9 xenopus lae
4	93.5	25.8	91	11 Q91ZL1	Q91ZL1 sigmodon hi
5	88	24.3	98	13 Q8QGV8	Q8QGV8 paraliichy
6	88	24.3	109	13 Q8QY59	Q8QY59 paraliichy
7	88	24.3	148	11 Q8QYD7	Q8QYD7 mus musculu
8	82.5	22.8	79	4 Q95689	Q95689 homo sapien
9	82.5	22.8	134	12 Q9YVA9	Q9YVA9 gallid herp
10	82.5	22.8	142	12 Q91BJ7	Q91BJ7 turkey herp
11	82	22.7	104	13 Q73912	Q73912 gallus galli
12	82	22.7	203	12 Q67634	Q67634 marek s dis
13	79.5	22.0	101	13 Q93442	Q93442 lampetra fl
14	79.5	22.0	108	6 Q28724	Q28724 oryctolagus
15	78	21.5	97	13 Q98TQ2	Q98TQ2 oncorhynch
16	77.5	21.4	97	6 Q9TTS6	Q9TTS6 bos taurus

17	76.5	21.1	100	11 Q91ZK9	Q91ZK9 sigmodon hi
18	76.5	21.1	101	11 Q91Z64	Q91Z64 sigmodon hi
19	76.5	21.1	363	13 Q90ZT0	Q90ZT0 brachydanio
20	76.5	21.1	1096	13 Q90ZT1	Q90ZT1 brachydanio
21	76	21.0	101	11 Q8UW91	Q8UW91 tritakis scy
22	76	21.0	106	11 Q92292	Q92292 cricetus
23	75.5	20.9	91	13 Q8Q556	Q8Q556 gallus galli
24	75.5	20.9	883	13 Q91493	Q91493 torpedo cal
25	74.5	20.6	97	13 Q8QFP5	Q8QFP5 cyprinus ca
26	73.5	20.3	97	11 Q92318	Q92318 cavia porce
27	73.5	20.3	126	11 Q99J60	Q99J60 mus musculu
28	73.5	20.3	601	13 Q73928	Q73928 scyllorhinu
29	72.5	20.0	95	12 Q98158	Q98158 keposi's sa
30	70	19.3	91	13 Q8Q557	Q8Q557 gallus galli
31	69.5	19.2	92	6 Q8S040	Q8S040 felis silve
32	69	19.1	80	4 Q1745	Q1745 homo sapien
33	69	19.1	93	4 Q96168	Q96168 homo sapien
34	69	19.1	93	13 Q90825	Q90825 gallus galli
35	69	19.1	395	11 Q91V44	Q91V44 mus musculu
36	68	18.8	89	13 Q918E0	Q918E0 gallus galli
37	68	18.8	102	6 Q95M27	Q95M27 ovis aries
38	67.5	18.6	101	11 Q9EP62	Q9EP62 ratius norv
39	67.5	18.6	116	11 Q91ZB2	Q91ZB2 mus musculu
40	67.5	18.6	1203	5 Q8T1J7	Q8T1J7 dictyostell
41	67.5	18.6	2994	5 Q95ZG5	Q95ZG5 dictyostell
42	67	18.5	62	4 Q95690	Q95690 homo sapien
43	66	18.2	92	11 Q91Z65	Q91Z65 sigmodon hi
44	66	18.2	100	6 Q95MD5	Q95MD5 bos taurus
45	65.5	18.1	100	13 Q8QGB7	Q8QGB7 oncorhynch

## ALIGNMENTS

RESULT 1	Q9H554	PRELIMINARY:	PRT:	92 AA.
ID	Q9H554			
AC	Q9H554			
DT	01-MAR-2001 (TRENBLREL. 16, Created)			
DT	01-MAR-2001 (TRENBLREL. 16, Last sequence update)			
DT	01-JUN-2002 (TRENBLREL. 21, Last annotation update)			
DE	BA20J15.1.2 (Stromal cell-derived factor 1, isoform beta)			
DE	(Fragment).			
GN	SDF1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Bird C.;			
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AL137026; CAC10202.1; -			
DR	HSSP; P48061; ISDF.			
DR	InterPro; IPR001811; Chemokine_IL8.			
DR	Pfam; PF00048; IL8; 1.			
DR	SMART; SM00199; SCY; 1.			
FT	NON_TER			
FT	SEQUENCE 92 AA: 10510 MW: AEF0C402B44ED20 CRC64;			
Query Match	95.6%: Score 346; DB 4; Length 92;			
Best Local Similarity	97.0%: Pred. No. 1.1e-35;			
Matches	65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	1 KGVSLPYRCPREFSHVARANKHLKINTPCALQIVARLKNNNRQVCIDPKLKIWE 60			
DB	22 KPVSLPYRCPREFSHVARANKHLKINTPCALQIVARLKNNNRQVCIDPKLKIWE 81			
QY	61 YLEKALN 67			
DB	82 YLEKALN 88			

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RESULT 2
Q90ZD1 PRELIMINARY; PRT; 89 AA.
ID 090ZD1
AC 090ZD1:
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Stromal cell-derived factor-1 alpha.
GN SDF-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SRRAIN-SPRAGUE-DAWLEY;
RA Ohtani Y., Okada M., Kawaguchi N., Minami M., Satoh M.;
RT "cDNA cloning of rat stromal cell-derived factor-1 alpha (SDF-1
alpha).";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Pillariseti K., Gupta S.K.;
RT "Identification and molecular cloning of a novel rat ortholog of the
RT alpha chemokine, stromal cell derived factor-1 (SDF-1).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF189724; AAF01066.1; -.
DR EMBL; AF209976; AAG43506.1; -.
DR HSSP; P48061; 1SDP.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCT; 1.
SQ SEQUENCE 89 AA; 9977 MW; D86977626A2E35FA CRC64;

Query Match 93.4%; Score 338; DB 11; Length 89;
Best Local Similarity 94.0%; Pred. No. 1,le-34;
Matches 63; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNQVCIIDPKLKIQIE 60
Db 22 KPVSLYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNQVCIIDPKLKIQIE 81
QY 61 YLEKALN 67
Db 82 YLDKALN 88

RESULT 3
Q80UJ9 PRELIMINARY; PRT; 94 AA.
ID 080UJ9;
AC 080UJ9;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Stromal-derived factor 1 precursor.
GN SDF-1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SPLEEN;
RA Braun M., Wunderlin M., Knoechel W., Gierschik P., Moepf B.;
RT "Xenopus laevis stromal-derived factor 1: conservation of structure
RT and function during vertebrate development.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; A2278857; CAC82196.1; -.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCT; 1.
KW Signal.

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FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 94 STROMAL-DERIVED FACTOR 1.
SQ SEQUENCE 94 AA; 10701 MW; 8C8325D152F326E7 CRC64;

Query Match 78.7%; Score 285; DB 13; Length 94;
Best Local Similarity 74.6%; Pred. No. 4,7e-28;
Matches 50; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 KGVSLPYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNQVCIIDPKLKIQIE 60
Db 22 KPVSLYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNQVCIIDPKLKIQIE 81
QY 61 YLEKALN 67
Db 82 YLEKALN 88

RESULT 4
Q91ZL1 PRELIMINARY; PRT; 91 AA.
ID 091ZL1
AC 091ZL1;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE RANTES chemokine.
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RA Bianco J.C., Pietreva L.M., Prince G.A.;
RT "Sigmodon hispidus cytokines, chemokines and interferons.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF421391; AAL16932.1; -.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; UNKNOWN.1.
SQ SEQUENCE 91 AA; 10082 MW; D0D6FAEABE4242ZF CRC64;

Query Match 25.8%; Score 93.5; DB 11; Length 91;
Best Local Similarity 38.2%; Pred. No. 0.00039;
Matches 21; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 10 PCRF--FESHVARANKHLKILNTPNCALQIVARLKNNNQVCIIDPKLKIQIEYL 62
Db 32 PCCFAYLSAVLPRAHKEY-FYTSKCSNFAVVFYTRNRHQCANPKKWOEYI 85

RESULT 5
Q80GV8 PRELIMINARY; PRT; 98 AA.
ID 080GV8;
AC 080GV8;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE CXC chemokine.
GN CXC CHEMOKINE.
OS Parachanna olivacea (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectidae; Parachthyidae; Parachthys.
OX NCBI_TaxID=8235;
RN [1]
RP SEQUENCE FROM N.A.
RA Aoki T., Hiroo I., Lee J., Iwahori A.;
RT "Molecular cloning and expression of IL-1b and two types of chemokines
RT in Japanese flounder, Parachthys olivacea.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB070837; BAB86884.1; -.

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SO SEQUENCE 198 AA: 10846 MW: 495CA4839A5D8C92 CRC64:
Query Match 24.3%; Score 86; DB 13; Length 98;
Best Local Similarity 31.9%; Pred. No. 0.002;
Matches 22; Conservative 17; Mismatches 24; Indels 6; Gaps 4;

OY 2 GVSFLPRCPRRFFESHVARANKYKHLKILNTPN--C-AIQVARKLNKNNRQVCIIDPKLKI 58
    |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 30 GVSFL--HRCRIETESPRIGRYIKSYVEII-SPNSHCDKTEIIATLKDGTGVELCLDPEAPWY 86

OY 59 OEYLEKALN 67
    : : | : :
Db 87 KRVIKKLIS 95

RESULT 6
O90Y59 PRELIMINARY: PRT: 109 AA.
AC O90Y59;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Interleukine-8.
GN IL-8.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectidae; Paralicthidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21435923; PubMed=11551708;
RA Lee E.Y., Park H.H., Kim Y.T., Chung J.K., Choi T.J.;
RT "Cloning and sequence analysis of the interleukin-8 gene from flounder
RT (Paralicthys olivaceus).";
RL Gene 274;237-243(2001).
DR EMBL; AF216646; AAL05442.1; -.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
SO SEQUENCE 109 AA: 12117 MW: C7CE18986C50A6ED CRC64:

Query Match 24.3%; Score 86; DB 13; Length 109;
Best Local Similarity 31.9%; Pred. No. 0.0023;
Matches 22; Conservative 17; Mismatches 24; Indels 6; Gaps 4;

OY 2 GVSFLPRCPRRFFESHVARANKYKHLKILNTPN--C-AIQVARKLNKNNRQVCIIDPKLKI 58
    |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 29 GVSFL--HRCRIETESPRIGRYIKSYVEII-SPNSHCDKTEIIATLKDGTGVELCLDPEAPWY 85

OY 59 OEYLEKALN 67
    : : | : :
Db 86 KRVIKKLIS 94

RESULT 7
O90YD7 PRELIMINARY: PRT: 148 AA.
AC O90YD7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Small inducible cytokine A2.
GN SCYA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=St/J; TISSUE=SPLEEN;
RX MEDLINE=99370037; PubMed=104389970.
RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,

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RA	Blankenhorn E.P.:
RT	"Sequence polymorphisms in the chemokines Sclay1 (TCA-3), Scyaz2
RT	(monocyte chemoattractant protein (MCP)-1), and Sclay2 (MCP-5) are
RT	candidates for eaey, a locus controlling susceptibility to monophasic
RT	remitting/nonrelapsing experimental allergic encephalomyelitis.";
RL	J. Immunol. 163:2267-2266(1999).
DR	EMBL; AF065929; AAF15379.1; -.
DR	HSSP; P13500; IDOK.
DR	MGI; MGI:98259; Scya2.
DR	InterPro; IPR000827; CC_chemkine_sml.
DR	InterPro; IPR001811; Chemokine_IL8.
DR	Pfam; PF000048; IL8; 1.
DR	SMART; SM00189; SCY; 1.
DR	PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ	SEQUENCE 148 AA; 16268 MW; 2BA24C5D19C489BD CRC64;
Query Match	24.3%; Score 88; DB 11; Length 148;
Best Local Similarity	26.6%; Pred. NO. 0.0031;
Matches 16; Conservative 14; Mismatches 31; Indels 0; Gaps 0;	
OY	3 VSLPRCCRFESHVAVRANKHLKLTLPNCALDIVARLKNNNROYCIDPKLKIOEYL 62
Dd	28 VNAPLTCGYSFASKIIPSRLEGYKRITSSRCPEAAVFVTKRKREVCADPKKEWQRYI 87
OY	63 E 63
Dd	88 K 88
RESULT 8	
OY5689	PRELIMINARY; PTR; 79 AA.
AC	O95689;
DT	01-MAY-1999 (TREMBLrel. 10, Created)
DT	01-MAY-1999 (TREMBLrel. 10, last sequence update)
DT	01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE	CC-Chemokine (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_Taxid=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=FORESKIN;
RA	Bartels J.H., Schlueter C., Richter E., Noso N., Christophers E.,
RA	Schroeder J.M.;
RT	"Expression of a MCP-4 like novel CC-chemokine in human dermal
RT	fibroblasts: molecular cloning and Rr-pcr analysis."
RL	Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.
DR	EMBL; Z77650; CAB0111.1; -.
DR	HSSP; P51671; IEOT.
DR	InterPro; IPR000827; CC_chemkine_sml.
DR	InterPro; IPR001811; Chemokine_IL8.
DR	Pfam; PF00048; IL8; 1.
DR	SMART; SM00199; SCY; 1.
DR	PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
FT	NON TER 1
SQ	SEQUENCE 79 AA; 8987 MW; 4FCF42983DA6C352 CRC64;
Query Match	22.8%; Score 82.5; DB 4; Length 79;
Best Local Similarity	28.6%; Pred. NO. 0.008;
Matches 18; Conservative 16; Mismatches 24; Indels 5; Gaps 3;	
OY	3 VSLPRCCRFESHVAVRANKHLK--ILNPNCALOIVARLKNNNROYCIDPKLKIOE 60
Dd	12 LNWPTGC-CETFS--KKISLDRLKSYYITTSRCPOKAVIFPTKLGLKICADPKKEKWON 68
OY	61 YLE 63
Dd	69 YMK *71
RESULT 9	

ID	Q91BA9	PRELIMINARY:	PRT:	134 AA.
AC	Q91BA9:			
DT	01-MAY-1999 (TREMBlrel. 10, Created)			
DT	01-MAY-1999 (TREMBlrel. 10, Last sequence update)			
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)			
DE	VIL8 (CXC chemokine VIL8).			
GN	MDV003 OR MDV078.			
OS	Gallid herpesvirus 1.			
OS	Marek's disease herpesvirus (strain GA) (MDHV), and			
OC	Marek's disease herpesvirus (strain MD5) (MDHV), Turkey herpesvirus.			
OC	viruses: dsDNA viruses, no RNA stage: Herpesviridae;			
OC	Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.			
OX	NCBI_TaxID=10386, 10388, 10389;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RC	SPECIES=Gallid herpesvirus 1; STRAIN=RB18;			
RA	Raschaert D., Fraquet L.;			
RT	"Characterisation of the BamHI I fragment of the Marek's disease virus			
RT	RB18 strain (serotype 1).";			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Marek's disease herpesvirus (strain GA) (MDHV);			
RA	Lin S.-F., Robinson D., Chen H.-C., Kung H.-T.;			
RT	"CXC chemokine encoded by Marek's Disease Virus (MDV).";			
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Marek's disease herpesvirus (strain MD5) (MDV);			
RX	MEDLINE=20392152; PubMed=10933706;			
RA	Tulman E.R., Alfonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;			
RT	"The genome of a very virulent Marek's disease virus.";			
RL	J. Virol. 74:7980-7988(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Marek's disease herpesvirus (strain MD5) (MDV);			
RA	Tulman E.R., Alfonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF314199; AAL58097.1; -			
DR	EMBL: AF065430; AAC77449.1; -			
DR	EMBL: AF243438; AAG14290.1; -			
DR	EMBL: AF243438; AAG14256.1; -			
DR	HSSP: P10889; 1MT2.			
DR	InterPro: IPR001811; Chemokine_IL8.			
DR	InterPro: IPR001089; CXC_chemokine_sm1.			
DR	PIfam: PF000048; IL8; 1.			
DR	PRINTS: PR00437; SMALLCYTRCXC.			
DR	SMART: SM00199; SCY: 1			
SO	SEQUENCE 134 AA; 14828 MW; C859CDB86BD25190 CRC64;			
	Query Match 22.8%; Score 82.5; DB 12; Length 134;			
	Best Local Similarity 27.5%; Pred. NO. 0.014;			
	Matches 22; Conservative 14; Mismatches 17; Indels 27; Gaps			
OY	2 GVSLEPRCPREFESHVAVANVKKHLKILNTP-----NC-AIQIYARLEKN 44			
DB	22 GISL-----ESLAVDRCKCKVQVTRPGLGIIVADVIAPGIIHCRRTETIPALK- 71			
OY	45 NNROYCIDIOPKLKIQEYLEK 64			
DB	72 NKRKYCVDEPAPWVOFFIKK 91			
RESULT	10			
Q91BA7				
ID	Q91BA7	PRELIMINARY:	PRT:	142 AA.
AC	Q91BA7:			
DT	01-OCT-2000 (TREMBlrel. 15, Created)			
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)			
DT	01-MAR-2002 (TREMBlrel. 20, Last annotation update)			
DE	VIL-8.			
GN	R-LORF2.			

OY	Turkey herpesvirus.
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
CC	Alphaherpesvirinae; Marek's disease-like viruses.
OX	NCBI_TaxID=10390;
ON	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-GA:
RX	MEDLINE=92237304; PubMed=1315048;
RA	Jones D., Lee L., Liu J.L., Kung H.J., Tillotson J.K.;
RT	"Marek disease virus encodes a basic-leucine zipper gene resembling the fos/jun oncogenes that is highly expressed in lymphoblastoid tumors.";
RL	Proc. Natl. Acad. Sci. U.S.A. 89:4042-4046(1992).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN-GA:
RA	Lee L.F., Wu P., Sui D., Ren D., Kung H.J.;
RT	"The complete ul sequence of Serotype I Marek's Disease Virus."
RL	Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2000).
DR	EMBL; AF147806; AAF67205.1; -
DR	EMBL; AF147806; AAF6793.1; -
DR	HSSB; P10889; IMI2.
DR	InterPro: IPRO01811; Chemokine_IIL8.
DR	InterPro: IPRO01089; CXC_chem_kine-sm1L.
DR	InterPro: IPRO01230; Prenyl_siste.
DR	Pfam; PF00048; IL8; 1.
DR	PRINTS; PR00437; SMALLCYTRKXC.
DR	SMART; SM00199; SCV; 1.
DR	PROSITE; PS00294; PRENYLATON; UNKNOWN.1.
SQ	SEQUENCE 142 AA; 15770 MW; 35A8CBB9B29FD209 CRC64;
	Query Match            22.8%; Score 82.5; DB 12; Length 142;
	Best Local Similarity     27.5%; Pred. No. 0.014;
	Matches 22; Conservative 14; Mismatches 17; Indels 27; Gaps
OY	2 GVSLPYRCPCRFFESHVARANKHKLINTP-----NC-AAGIVARLKN 44
	:   :   :
DB	22 GSLSL-----ESLAVDCKCKVKVTNPGLGPIIAVDVIPPGIHCRRTTIFALK- 71
OY	45 NNROYCIDPKLKWIOEYLEEK 64
	:  :  : ::
DB	72 KNKKVCVPDEAPWVOGFIRK 91
RESULT 11	
ID	073912
AC	PRELIMINARY;        PRT;      104 AA.
AD	073912:
DT	01-AUG-1998 (TREMBLrel. 07, Created)
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT	01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE	K60 protein precursor (CXC chemokine K60).
CN	K60.
OS	Gallus gallus (chicken).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC	Gallus.
OX	NCBI_TaxID=9031;
ON	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=MACROPHAGE LIKE;
RA	SICK C.;
RN	submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20170941; PubMed=10704244;
RA	Slick C., Schneider K., Staeheli P., Welting K.C.;
RT	"Novel chicken CXC and CC chemokines.";
RL	Cytokine 12:181-186(2000).
RN	[3]
RP	SEQUENCE FROM N.A.
RE	Hughes S.M., Bunnstead N.;
RT	"Mapping of a second ELR CXC chemokine to chicken chromosome four.";



Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Y14971; CAA75212.1; -  
 DR EMBL: AF277660; AAF65485.1; -  
 DR HSSP: P02775; ITVX.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR InterPro: IPR001089; CXC\_chemkine\_sml1.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTKXC.  
 DR SMART: SM00199; SCY; 1.  
 DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; 1.  
 DR Signal.  
 FT SIGNAL. 1 20  
 FT CHAIN 21 104 POTENTIAL.  
 FT CHAIN 21 104 K60 PROTEIN.  
 SQ SEQUENCE 104 AA; 11199 MW; 83725AB91FE18E3D CRC64;  
 Query Match 22.7%; Score 82; DB 13; Length 104;  
 Best Local Similarity 27.5%; Pred. No. 0.012;  
 Matches 19; Conservative 20; Mismatches 22; Indels 8; Gaps 4;  
 Oy 4 SLPPRCRPFESHVARANKHLKILNT---PNCALQIVARLKNNNROVCIIDPKLKI 58  
 Db 29 ALELRKQC--IEHRSKFIHKFQIYNVNLTPSGHCANVEVIATLK-DGREVCUDPTAPV 85  
 Oy 59 OEYLEKALN 67  
 Db 86 KLITKALD 94  
 RESULT 12  
 ID 067634 PRELIMINARY; PRT; 203 AA.  
 AC 067634;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Eco Q protein (Fragment).  
 OS Marek's disease herpesvirus (strain GA) (MDHV).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Marek's disease-like viruses.  
 OX NCBI\_TaxID=10388;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-GA;  
 RX MEDLINE-96074534; PubMed-7491783;  
 RA Peng Q., Zeng M., Bhulian Z.A., Ubukata E., Tanaka A., Nonoyama M., Shitazaki Y.;  
 RA "Isolation and characterization of Marek's disease virus (MDV) cDNAs mapping to the BamHI-12, BamHI-Q2, and BamHI-L fragments of the MDV genome from lymphoblastoid cells transformed and persistently infected with MDV.";  
 RT Virology 213:590-599(1995).  
 RL EMBL: U34966; AAC54629.1; -  
 DR HSSP: P10889; IMI2.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR InterPro: IPR001089; CXC\_chemkine\_sml1.  
 DR InterPro: IPR004827; TF\_bZIP.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTKXC.  
 DR SMART: SM00338; BRLZ; 1.  
 DR SMART: SM00199; SCY; 1.  
 FT NON\_TER 1 1  
 FT SEQUENCE 203 AA; 23132 MW; DEA2F2A1C1A71C88 CRC64;  
 Query Match 22.7%; Score 82; DB 12; Length 203;  
 Best Local Similarity 23.5%; Pred. No. 0.024;  
 Matches 19; Conservative 17; Mismatches 13; Indels 32; Gaps 4;  
 Oy 1 KGVSLPPRCRPFESHVARANKHLKILNT-----NCALQIVARLK 43  
 Db 95 ESIAVAKRCG-----VKVTRPTGLPIIAVDVIPPICHCRTTEIIFALK 140  
 Oy 44 NNRQVCIDPKLKIOWYLEK 64  
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Db 141 -KNRKCVDPEAPWQOFIKK 160  
 RESULT 13  
 ID 093442 PRELIMINARY; PRT; 101 AA.  
 AC 093442;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE LfCA-1 protein precursor.  
 OS Lampetra fluviatilis (River lamprey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
 OC Petromyzontiformes; Petromyzontidae; Lampetra.  
 OX NCBI\_TaxID=7748;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LEUKOCYTES;  
 RA Nakashin A.M., Mechelina L.V., Alabyev B.Y., Taranin A.V.;  
 RT "Identification of the interleukin 8 homologue in lamprey (Lampetra fluviatilis): early evolutionary divergence of chemokines.";  
 RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AJ231072; CAA13114.1; -  
 DR HSSP: P02775; ITVX.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR InterPro: IPR001089; CXC\_chemkine\_sml1.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTKXC.  
 DR SMART: SM00199; SCY; 1.  
 DR Signal.  
 FT SIGNAL. 23 101  
 FT CHAIN 23 101 LfCA-1 PROTEIN.  
 SQ SEQUENCE 101 AA; 11095 MW; 80CFEE81EA7336D2 CRC64;  
 Query Match 22.0%; Score 79.5; DB 13; Length 101;  
 Best Local Similarity 26.9%; Pred. No. 0.024;  
 Matches 18; Conservative 16; Mismatches 22; Indels 11; Gaps 4;  
 Oy 8 RCRPCRFESHVARANKHLK----LNTPNCA-LQIVARLKNNNROVCIIDPKLKIOW 60  
 Db 30 RCOC---VHVISKFIHKFQIYNVNLTPSGHCANVEVIATMKSTNQICLNDAVVRK 85  
 Oy 61 YLEKALN 67  
 Db 86 VISHILD 92  
 RESULT 14  
 ID 028724 PRELIMINARY; PRT; 108 AA.  
 AC 028724;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-AUG-1999 (TREMBlrel. 11, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE GRO (Permeability factor 2).  
 GN RPF2.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NEW ZEALAND WHITE;  
 RA Yoshimura T., Modi W.S.;  
 RT "Isolation of novel GRO genes, and a phylogenetic analysis of the CXC chemokine subfamily in mammals.";  
 RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 43-108 FROM N.A.  
 RC STRAIN=NEW ZEALAND WHITE;  
 RX MEDLINE-95129889; PubMed-7828903;  
 RA Johnson M.C., Goodman R.B. II, Kajikawa O., Wong V.A., Mongovin S.M., Martin T.R.;

RT "Cloning of two rabbit GRO homologues and their expression in alveolar  
 RT macrophages."  
 RL Gene 151:337-338(1994).  
 DR EMBL: U95808: AAB93924.1; -  
 DR EMBL: L28933: AAB66975.1; -  
 DR HSSP: P19875: 10NK.  
 DR InterPro: IPR001811: Chemokine\_IL8.  
 DR InterPro: IPR001089: CXCL12-chemokine\_sm11.  
 DR Pfam: PF00048: IL8; 1.  
 DR PRINTS: PR00437: SMALLCYTFCXC.  
 DR SMART: SM00199: SCY; 1.  
 DR PROSITE: PS00471: SMALL\_CYTOKINES\_CXC; 1.  
 SQ SEQUENCE 108 AA; 11261 MW; 9C278041FC7A5BAD CRC64;

Query Match 22.0%; Score 79.5; DB 6; Length 108;  
 Best Local Similarity 27.4%; Pred. No. 0.026;  
 Matches 17; Conservative 21; Mismatches 21; Indels 3; Gaps 3;

QY 8 RCPGRFESHVARNVHKLINT-NTPCA-LQIVARLKNNNROYCIDPKLKIQEYLEKA 65  
 Db 43 RCQCLQTVGGIHLKSIQSLKVLSPGHCQTEVIATLK-SQGEACLNPAAPMVKKFLQKR 101  
 QY 66 LN 67  
 Db 102 LS 103

## RESULT 15

098T02 PRELIMINARY; PRT; 97 AA.

AC 098T02; 01-JUN-2001 (TREMUREL. 17, Created)

DT 01-JUN-2001 (TREMUREL. 17, Last sequence update)

DT 01-JUN-2002 (TREMUREL. 21, Last annotation update)

DE Putative interleukin 8 (Putative cxc chemokine precursor).

GN IL-8.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI\_TaxID=8022;

RN [1]

RP SEQUENCE FROM N.A.\*

RA Laing K.J., Zou J.J., Hirono I., Aoki T., Secombes C.J.;

RT "Identification and analysis of the interleukin 8 molecule in rainbow

trout Oncorhynchus mykiss."

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=KIDNEY;

RA Sangrador-Vegas A., Smith T.J.;

RT "Molecular cloning of a rainbow trout (Oncorhynchus mykiss) CXC

chemokine by use of suppression subtractive hybridization."

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Laing K.J., Zou J.J., Hirono I., Aoki T., Secombes C.J.;

RT "Identification and analysis of the interleukin 8 molecule in rainbow

trout Oncorhynchus mykiss."

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ279069; CAC33585.1; -

DR EMBL: AJ300835; CAC45061.1; -

DR EMBL: AJ310565; CAC83945.1; -

DR HSSP: P19875: 10NK.

DR InterPro: IPR001811: Chemokine\_IL8.

DR InterPro: IPR001089: CXCL12-chemokine\_sm11.

DR Pfam: PF00048: IL8; 1.

DR PRINTS: PR00437: SMALLCYTFCXC.

DR SMART: SM00199: SCY; 1.

KM SIGNAL.

FT SIGNAL. 1 22 POTENTIAL.

FT CHAIN 23 97 PUTATIVE CXC CHEMOKINE.

SQ SEQUENCE 97 AA; 10777 MW; 4EBB35A4EF9DACE2 CRC64;

Query Match 21.5%; Score 78; DB 13; Length 97;  
 Best Local Similarity 25.0%; Pred. No. 0.036;  
 Matches 17; Conservative 18; Mismatches 31; Indels 2; Gaps 2;

QY 1 KGVSLEPYRCPCRFESHVARNVHKLINT-NTPCA-LQIVARLKNNNROYCIDPKLKI 58  
 Db 26 RGMGADLRRCRCIETESRRIGRLIKRVEMFPSSHCRTETIATLSKSGEICLDVSA 85  
 QY 59 QEYLEKAL 66  
 Db 86 KRVIEKML 93

Search completed: January 23, 2003, 15:36:20  
 Job time : 23.6 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 23, 2003, 15:27:48 ; Search time 28.2 Seconds  
(without alignments)  
316.588 Million cell updates/sec

Title: US-09-852-424-4

Perfect score: 359  
Sequence: 1 KGVSLSPRCPCRFPSHVAR.....QVCIDPKLKIQETLEKALN 67

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	349	97.2	67	23	AA1981.DAT
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4	342	95.3	67	23	AA1983.DAT
5	342	95.3	67	23	AA1984.DAT
6	341	95.0	67	19	AA1985.DAT
7	341	95.0	67	20	AA1986.DAT
8	341	95.0	67	20	AA1987.DAT
9	341	95.0	67	20	AA1988.DAT
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13	341	95.0	69	20	AA1992.DAT
14	341	95.0	72	19	AA1993.DAT
15	341	95.0	72	21	AA1994.DAT
16	341	95.0	72	21	AA1995.DAT
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19	341	95.0	74	21	AA1998.DAT
20	341	95.0	89	16	AA1999.DAT
21	341	95.0	89	20	AA2000.DAT
22	341	95.0	89	20	AA2001.DAT
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28	341	95.0	93	19	AA2007.DAT
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33	341	95.0	93	23	AA2012.DAT
34	341	95.0	93	23	AA2013.DAT
35	341	95.0	93	23	AA2014.DAT
36	341	95.0	94	20	AA2015.DAT
37	341	95.0	101	23	AA2016.DAT
38	341	95.0	119	23	AA2017.DAT
39	341	95.0	166	20	AA2018.DAT
40	341	95.0	177	20	AA2019.DAT
41	341	95.0	320	21	AA2020.DAT
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/note="Optionally the proline analogue 6-amino-7-oxo-2,3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic acid residue or a bicyclic turned dipeptide (Btd)"

WO200185196-A2.	
15-NOV-2001.	
09-MAY-2001: 2001WO-CA00659.	
09-MAY-2000: 2000CA-2305787.	
19-MAY-2000: 2000US-205467P.	
(UYBR-) UNIV BRITISH COLUMBIA.	

PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 XX Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;  
 PI Clark-Lewis I, Salari H;  
 XX  
 DR WPI; 2002-106073/14.  
 XX  
 PT Promoting the rate of haematopoietic cell multiplication for treating a  
 PT cancer involves administering chemokine receptor antagonist to the  
 PT cells -  
 XX  
 PS Claim 9; Page 54; 68pp; English.  
 XX  
 CC The invention relates to a method of promoting the rate of haematopoietic  
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)  
 CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist  
 CC has cytostatic and immunosuppressive activity and is useful for treating  
 CC cancer or autoimmune disease in a patient; to promote the rate of  
 CC haematopoietic cell multiplication; to formulate a medicament for  
 CC increasing the circulation of the haematopoietic cells in a patient; for  
 CC mobilising haematopoietic cells from a narrow locus to a peripheral blood  
 CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The  
 CC CXCR4 antagonists stimulates haematopoietic cell multiplication,  
 CC self-renewal, expansion and proliferation of peripheralisation in vivo.  
 CC  
 XX  
 SQ Sequence 67 AA;  
 Query Match 100.0%; Score 359; DB 23; Length 67;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-39;  
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KGVSLSPRCPCRFESHVARANKHLKILTPNCALQIVARLKNNRQVCIDPKLKWIOE 60  
 Db 1 KGVSLSPRCPCRFESHVARANKHLKILTPNCALQIVARLKNNRQVCIDPKLKWIOE 60  
 QY 61 YLEKALN 67  
 Db 61 YLEKALN 67  
 Db 61 YLEKALN 67

RESULT 2  
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 ID AAM48656 standard; peptide; 67 AA.  
 AC AAM48656;  
 XX  
 DT 20-MAY-2002 (first entry)  
 DE CXCR4 peptide antagonist SEQ ID NO 1.  
 XX  
 KW CRCX4; haematopoietic cell; chemokine receptor-4; cytostatic;  
 KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;  
 KM cell multiplication.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200185196-A2.  
 PD 15-NOV-2001.  
 PF 09-MAY-2001; 2001WO-CA00659.  
 XX  
 PR 09-MAY-2000; 2000CA-2305787.  
 PR 19-MAY-2000; 2000US-205467P.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 XX  
 PI Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;  
 PI Clark-Lewis I, Salari H;  
 XX  
 DR WPI; 2002-106073/14.  
 XX

PT Promoting the rate of haematopoietic cell multiplication for treating a  
 PT cancer involves administering chemokine receptor antagonist to the  
 PT cells -  
 XX  
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 XX  
 CC The invention relates to a method of promoting the rate of haematopoietic  
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)  
 CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist  
 CC has cytostatic and immunosuppressive activity and is useful for treating  
 CC cancer or autoimmune disease in a patient; to promote the rate of  
 CC haematopoietic cell multiplication; to formulate a medicament for  
 CC increasing the circulation of the haematopoietic cells in a patient; for  
 CC mobilising haematopoietic cells from a narrow locus to a peripheral blood  
 CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The  
 CC CXCR4 antagonists stimulates haematopoietic cell multiplication,  
 CC self-renewal, expansion and proliferation of peripheralisation in vivo.  
 CC  
 XX  
 SQ Sequence 67 AA;  
 Query Match 97.2%; Score 349; DB 23; Length 67;  
 Best Local Similarity 98.5%; Pred. No. 3.5e-38;  
 Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 KGVSLSPRCPCRFESHVARANKHLKILTPNCALQIVARLKNNRQVCIDPKLKWIOE 60  
 Db 1 KGVSLSPRCPCRFESHVARANKHLKILTPNCALQIVARLKNNRQVCIDPKLKWIOE 60  
 QY 61 YLEKALN 67  
 Db 61 YLEKALN 67  
 Db 61 YLEKALN 67

RESULT 3  
 AAM48658  
 ID AAM48658 standard; peptide; 67 AA.  
 AC AAM48658;  
 XX  
 DT 20-MAY-2002 (first entry)  
 DE CXCR4 peptide antagonist SEQ ID NO 3.  
 XX  
 KW CRCX4; haematopoietic cell; chemokine receptor-4; cytostatic;  
 KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;  
 KM cell multiplication.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200185196-A2.  
 PD 15-NOV-2001.  
 PF 09-MAY-2001; 2001WO-CA00659.  
 XX  
 PR 09-MAY-2000; 2000CA-2305787.  
 PR 19-MAY-2000; 2000US-205467P.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 XX  
 PI Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;  
 PI Clark-Lewis I, Salari H;  
 XX  
 DR WPI; 2002-106073/14.  
 XX

Key Location/Qualifiers  
 Modified-site 6  
 /note="optionally the proline analogue 6-amino-7-oxo-2,3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic acid residue or a bicyclic turned dipeptide (Btd)"

PT Promoting the rate of haematopoietic cell multiplication for treating a  
PT cancer involves administering chemokine receptor antagonist to the  
PT cells -  
PS Claim 9; Page 54; 68pp; English.  
XX  
XX  
XX The invention relates to a method of promoting the rate of haematopoietic  
CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)  
CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist  
CC has cytostatic and immunosuppressive activity and is useful for treating  
CC cancer or autoimmune disease in a patient; to promote the rate of  
CC haematopoietic cell multiplication; to formulate a medicament for  
CC increasing the circulation of the haematopoietic cells in a patient; for  
CC mobilising haematopoietic cells from a narrow locus to a peripheral blood  
CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The  
CC CXCR4 antagonists stimulates haematopoietic cell multiplication,  
CC self-renewal, expansion and proliferation of peripheralisation in vivo.  
XX  
XX Sequence 67 AA:  
SQ  
Query Match 95.8%; Score 344; DB 23; Length 67;  
Best Local Similarity 97.0%; Pred. No. 1.6e-37;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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DB 1 KGVSLPYRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60  
QY 61 YLEKALN 67  
DB 61 YLEKALN 67  
RESULT 4  
AAM48657  
ID AAM48657 standard; peptide: 67 AA.  
XX  
XX AAM48657;  
AC  
XX 20-MAY-2002 (first entry)  
DT  
XX  
XX CXCR4 peptide antagonist SEQ ID NO 2.  
DE  
XX  
XX CRCK4: haematopoietic cell; chemokine receptor-4; cytostatic;  
KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;  
KW cell multiplication.  
XX  
XX Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
FH Modified-site 5  
FT /note= "Optionally the proline analogue 6-amino-7-oxo-2,  
FT 3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic  
FT acid residue or a bicyclic turned dipeptide  
FT (Bcd)"  
XX  
XX WO200185196-A2.  
PN  
XX  
XX 15-NOV-2001.  
PD  
XX  
XX 09-MAY-2001; 2001WO-CA00659.  
PF  
XX  
XX 09-MAY-2000; 2000CA-2305787.  
PR  
XX  
XX 19-MAY-2000; 2000US-205467P.  
PR  
XX  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
XX  
XX Tuden CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;  
PI Clark-Lewis I, Salari H;  
XX  
XX WPI; 2002-106073/14.  
DR  
XX  
XX

PT Promoting the rate of haematopoietic cell multiplication for treating a  
PT cancer involves administering chemokine receptor antagonist to the  
PT cells -  
PS Claim 9; Page 54; 68pp; English.  
XX  
XX  
XX The invention relates to a method of promoting the rate of haematopoietic  
CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)  
CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist  
CC has cytostatic and immunosuppressive activity and is useful for treating  
CC cancer or autoimmune disease in a patient; to promote the rate of  
CC haematopoietic cell multiplication; to formulate a medicament for  
CC increasing the circulation of the haematopoietic cells in a patient; for  
CC mobilising haematopoietic cells from a narrow locus to a peripheral blood  
CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The  
CC CXCR4 antagonists stimulates haematopoietic cell multiplication,  
CC self-renewal, expansion and proliferation of peripheralisation in vivo.  
XX  
XX Sequence 67 AA:  
SQ  
Query Match 95.3%; Score 342; DB 23; Length 67;  
Best Local Similarity 97.0%; Pred. No. 2.9e-37;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 KGVSLSPRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60  
DB 1 KGVSLPYRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNNROYCIDPKLWIOE 60  
QY 61 YLEKALN 67  
DB 61 YLEKALN 67  
RESULT 5  
AAM48660  
ID AAM48660 standard; peptide: 67 AA.  
XX  
XX AAM48660;  
AC  
XX 20-MAY-2002 (first entry)  
DT  
XX  
XX CXCR4 peptide antagonist SEQ ID NO 5.  
DE  
XX  
XX CRCK4: haematopoietic cell; chemokine receptor-4; cytostatic;  
KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;  
KW cell multiplication.  
XX  
XX Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
FH Modified-site 8  
FT /note= "Optionally the proline analogue 6-amino-7-oxo-2,  
FT 3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic  
FT acid residue"  
FT  
XX  
XX WO200185196-A2.  
PN  
XX  
XX 15-NOV-2001.  
PD  
XX  
XX 09-MAY-2001; 2001WO-CA00659.  
PF  
XX  
XX 09-MAY-2000; 2000CA-2305787.  
PR  
XX  
XX 19-MAY-2000; 2000US-205467P.  
PR  
XX  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
XX  
XX Tuden CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;  
PI Clark-Lewis I, Salari H;  
XX  
XX WPI; 2002-106073/14.  
DR  
XX  
XX Promoting the rate of haematopoietic cell multiplication for treating a

PT cancer involves administering chemokine receptor antagonist to the  
 PT cells -  
 PS Claim 9: Page 54; 68pp; English.  
 XX  
 CC The invention relates to a method of promoting the rate of hematopoietic  
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)  
 CC antagonist (AA48656-AA48701) to hematopoietic cells. The antagonist  
 CC has cytostatic and immunosuppressive activity and is useful for treating  
 CC cancer or autoimmune disease in a patient; to promote the rate of  
 CC hematopoietic cell multiplication; to formulate a medicament for  
 CC increasing the circulation of the hematopoietic cells in a patient; for  
 CC mobilising hematopoietic cells from a marrow locus to a peripheral blood  
 CC locus; in the treatment of hematopoietic cells in vitro and in vivo. The  
 CC CXCR4 antagonists stimulates hematopoietic cell multiplication,  
 CC self-renewal, expansion and proliferation of peripheralisation in vivo.  
 CC  
 SQ Sequence 67 AA:  
 Query Match 95.3%; Score 342; DB 23; Length 67;  
 Best Local Similarity 97.0%; Pred. No. 2.9e-37;  
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 KGVSLSPRCPCRFESHVARANKHLKILNTPNCALQIVARLKNRQVCIDPKLKWIOE 60  
 DB 1 KGVSLSPRCPCRFESHVARANKHLKILNTPNCALQIVARLKNRQVCIDPKLKWIOE 60  
 OY 61 YLEKALN 67  
 DB 61 YLEKALN 67  
 RESULT 6  
 AA50760  
 ID AA50760 standard; peptide; 67 AA.  
 XX  
 AC AA50760:  
 XX  
 DT 27-JUL-1998 (first entry)  
 XX  
 DE Peptide which binds to CXCR4 receptor and is useful for treating HIV.  
 XX  
 KW Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus;  
 KW HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN FR2751658-A1.  
 XX  
 PD 30-JAN-1998.  
 XX  
 PF 26-JUL-1996; 96FR-0009477.  
 XX  
 PR 26-JUL-1996; 96FR-0009477.  
 XX  
 PA (INSP ) INST PASTEUR.  
 XX  
 PI Arenzana SF, Baggiolini M, Clark LI, Moser B, Virelizier JL;  
 XX  
 DR WPI: 1998-123039/12.  
 XX  
 PT Human stromal cell-derived chemokine, SDF-1 - useful for treating  
 PT human immunodeficiency virus infection  
 XX  
 PS Claim 2: Page 29; 48pp; French.  
 XX  
 CC The invention relates to peptides which bind to a cellular receptor for  
 CC CXC chemokines, namely the CXCR4 receptor (also known as leukocyte-  
 CC expressed transmembrane domain receptor), especially where the  
 CC peptide is human chemokine SDF-1. The peptide can be used to treat or  
 CC prevent HIV infections, optionally together with reverse transcriptase  
 CC inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4  
 CC receptor antagonists, immunotherapy agents, agents for treating HIV.

CC associated opportunistic infections and/or other CXC or CC chemokines,  
 CC especially RANTES, MIP1- alpha , MIP1- beta or MCP1. The peptide can be  
 CC used to detect anti-SDF-1 antibodies in biological fluids. This  
 CC sequence represents a specifically claimed peptide which binds to the  
 CC CXCR4 receptor.  
 CC  
 SQ Sequence 67 AA:  
 Query Match 95.0%; Score 341; DB 19; Length 67;  
 Best Local Similarity 97.0%; Pred. No. 3.9e-37;  
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 KGVSLSPRCPCRFESHVARANKHLKILNTPNCALQIVARLKNRQVCIDPKLKWIOE 60  
 DB 1 KPVSLSPRCPCRFESHVARANKHLKILNTPNCALQIVARLKNRQVCIDPKLKWIOE 60  
 OY 61 YLEKALN 67  
 DB 61 YLEKALN 67  
 RESULT 7  
 AA34092  
 ID AA34092 standard; protein; 67 AA.  
 XX  
 AC AA34092:  
 XX  
 DT 29-NOV-1999 (first entry)  
 XX  
 DE Native stromal cell derived factor 1 (SDF-1) alpha protein.  
 XX  
 KW CXC chemokine receptor 4; CXCR4; antagonist; medicament; T-cell;  
 KW Interferon gamma; autoimmune disease; multiple sclerosis; cancer;  
 KW angiogenesis; stromal cell derived factor 1; SDF-1.  
 XX  
 OS Mammalia.  
 XX  
 PN WO9947158-A2.  
 XX  
 PD 23-SEP-1999.  
 XX  
 PF 12-MAR-1999; 99WO-CA00221.  
 XX  
 PR 13-MAR-1998; 98CA-2226391.  
 PR 14-AUG-1998; 98CA-2245224.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX  
 XX  
 PI Clark-Lewis I, Gong J, Duronio V;  
 XX  
 DR WPI: 1999-561857/47.  
 XX  
 PT Use of CXC chemokine receptor 4 for treating autoimmune disease and  
 PT cancer -  
 XX  
 PS Example 1: Fig 1; 71pp; English.  
 XX  
 CC The invention relates to the use of a CXC chemokine receptor 4 (CXCR4)  
 CC antagonist for the manufacture of a medicament for reducing interferon  
 CC gamma production by T-cells in a mammal. The CXCR4 antagonist can be used  
 CC to treat or to design a medicament to treat, an autoimmune disease,  
 CC multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4  
 CC antagonists may be peptide compounds comprising a substantially purified  
 CC peptide fragment, analogue or a pharmacologically acceptable salt of  
 CC stromal cell derived factor 1 (SDF-1). The present sequence represents  
 CC the amino acid sequence of SDF-1 alpha protein.  
 CC  
 SQ Sequence 67 AA:  
 Query Match 95.0%; Score 341; DB 20; Length 67;  
 Best Local Similarity 97.0%; Pred. No. 3.9e-37;  
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



Db 61 YLEKALN 67

RESULT 10  
AA67594

ID AAY67594 standard; peptide; 67 AA.

AC AAY67594;

DT 13-JUN-2000 (first entry)

DE SDF-1alpha peptide sequence.

XX SDF-1; CXCR4; CXC chemokine receptor 4; gamma-interferon; cancer; gout;  
KM autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;  
KM type 1 diabetes; ulcerative colitis; lupus; antagonist; antitumour;  
KW stromal cell derived factor one; anti-inflammatory; immunomodulatory.

XX Unidentified.

PN W0200009152-A1.

PD 24-FEB-2000.

PF 16-AUG-1999; 99WO-CA00750.

PR 14-AUG-1998; 98CA-2245224.

PA (UYBR-) UNIV BRITISH COLUMBIA.

PI Clark-Lewis I, Gong J, Duronio V, Salari H;

DR WPI; 2000-224175/19.

XX Therapeutic composition containing CXCR4 antagonist, useful for  
PT treating autoimmune disease, especially multiple sclerosis and cancer  
PT

PS Disclosure; Fig 1; 88pp; English.

XX The invention provides a therapeutic composition containing an antagonist  
CC of CXCR4 (CXC chemokine receptor 4) and an excipient. The compositions  
CC are specifically used: to reduce production of gamma-interferon by T  
CC cells, particularly for treating autoimmune disease, especially multiple  
CC sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral  
CC sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative  
CC colitis, gout, lupus and transplant rejection; to treat cancer by  
CC inhibiting angiogenesis; inhibition of restenosis; and when labeled, to  
CC evaluate in vivo pharmacokinetics, or to determine disease progression  
CC and susceptibility, or as targeting agents for delivery of other  
CC therapeutic agents. The antagonist is selected from SDF-1 (stromal cell  
CC derived factor one) peptide fragments, SDF-1 being the only known natural  
CC ligand for CXCR4. The present sequence represents a SDF-1alpha  
CC peptide sequence.  
CC

SQ Sequence 67 AA;

Query Match 95.0%; Score 341; DB 21; Length 67;

Best Local Similarity 97.0%; Pred. No. 3.9e-37;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSPRCPCRFESHVARANVYHKLILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

Db 1 KPVSLSTRCPCCRFESHVARANVYHKLILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

QY 61 YLEKALN 67

Db 61 YLEKALN 67

RESULT 11  
AAB47680

ID AAB47680 standard; peptide; 67 AA.  
XX  
XX AAB47680;

DT 30-JAN-2002 (first entry)

DE SDF-1-alpha.

XX Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4;  
KM agonist; stromal cell derived factor one; SDF-1; autoimmune disease;  
KM macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;  
KW autologous; allogenic; bone marrow; stem cell; transplantation.

XX Homo sapiens.

PN W0200176615-A2.

PD 18-OCT-2001.

PF 12-APR-2001; 2001WO-CA00540.

PR 12-APR-2000; 2000CA-2305036.

PR 14-SEP-2000; 2000US-232425P.

PR 23-FEB-2001; 2001CA-2335109.

PA (UYBR-) UNIV BRITISH COLUMBIA.  
(CHEM-) CHEMOKINE THERAPEUTICS CORP.

PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;

DR Cashman J, Clark-Lewis I;

DR WPI; 2002-025882/03.

XX CXC receptor 4 agonists that reduces hematopoietic cell multiplication  
PT and susceptibility to cytotoxic agents, are useful for bone marrow or  
PT peripheral blood stem cell transplantation  
PT

PS Claim 8; Page 57; 74pp; English.

XX The sequences given in AAB47680-717 represent peptides which may be  
CC used in the method of the invention for reducing the rate of  
CC hematopoietic cell multiplication. These peptides act as CXC chemokine  
CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on  
CC stromal cell derived factor one (SDF-1) with some also containing  
CC sequences derived from macrophage inflammatory protein 1-alpha  
CC (MIP-1-alpha). They can be used to reduce susceptibility of  
CC hematopoietic cells to a cytotoxic agent, by administering one of the  
CC agonist peptides to the cells prior to or during exposure of the  
CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce  
CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly  
CC in a patient with cancer requiring autologous or allogenic bone marrow  
CC or peripheral blood stem cell transplantation, or an autoimmune disease.  
CC

SQ Sequence 67 AA;

Query Match 95.0%; Score 341; DB 23; Length 67;

Best Local Similarity 97.0%; Pred. No. 3.9e-37;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSPRCPCRFESHVARANVYHKLILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

Db 1 KPVSLSTRCPCCRFESHVARANVYHKLILTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

QY 61 YLEKALN 67

Db 61 YLEKALN 67

RESULT 12  
AAM50761  
ID AAM50761 standard; peptide; 68 AA.  
XX  
XX AAM50761;



[illegible][illegible]





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      82 YLEKALN 88
Db

```

RESULT 2  
US-08-674-008-1

Sequence 1 Application US/08674008  
Patent No. 5756084  
GENERAL INFORMATION:  
APPLICANT: HONJO, Tasuku  
APPLICANT: SHIROZU Michio  
APPLICANT: TADA, Hideaki  
TITLE OF INVENTION: HUMAN STROMAL DERIVED  
TITLE OF INVENTION: FACTOR 1' AND 1 (As Amended)  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SUGHRE, MION, ZINN, MACPEAK & SEAS  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/674, 008  
FILING DATE: 1-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/323,084  
FILING DATE: 14-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 280505/1993  
FILING DATE: 14-OCT-1993  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 89 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
OS-08-674-008-1

```

Query Match          95.0%:  Score 341:  DB 1:  Length 89:
Best Local Similarity 97.0%:  Pred. No. 1.9e-37:
Matches 65:  Conservative 0:  Mismatches 2:  Indels 0:  Gaps 0

QY      1  KGVLSIPRCRFEFESHVARANVKHLKITLNPNCALQIVARLKNNNROYCIDPKLWIG 60
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      22  KPVLSIYRCPCRFESHVARANVKHLKITLNPNCALQIVARLKNNNROYCIDPKLWIG 81
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY      61  YLEKALN 67
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      82  YLEKALN 88

RESULT 3
US-08-323-084A-5
: Sequence 5, Application US/08323084A
: Patent No. 5563048
: GENERAL INFORMATION:
: APPLICANT: HONJO, TASUKU
: APPLICANT: SHIROZU, MICHIO
: APPLICANT: TADA, HIDEAKI
: TITLE OF INVENTION: No. 5563048e1 Polypeptides and DNAs encoding them
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:

```

```

ADDRESSSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,084A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 280505/1993
FILING DATE: 14-OCT-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-323-084A-5

Query Match          95.0%; Score 341; DB 1; Length 93;
Best Local Similarity 97.0%; Pred. No. 2e-37;
Matches    65; Conservative   0; Mismatches    2; Indels     0; Gaps      0

QY      1 KGVSLSPKPCRFESHVAVANVKHLILNPNCALQIVARLKNRRROYCIDPKLKWIG 60
        |||||
Db       22 KPVSLSYNCPCRFESHVAVANVKHLILNPNCALQIVARLKNRRRCYCIPDKLKWIG 81
QY      61 YLEKALN 67
        |||||
Db       82 YLEKALN 88

RESULT 4
US-08-674-008-5
Sequence 5, Application US/08674008
Patent No. 5756084
GENERAL INFORMATION:
APPLICANT: HONJO, Tasuku
APPLICANT: SHIROZU, Michio
APPLICANT: TADA, Hideaki
TITLE OF INVENTION: HUMAN STROMAL DERIVED
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/674,008
FILING DATE: 1-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,084
FILING DATE: 14-OCT-1994

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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 280505/1993  
FILING DATE: 14-OCT-1993  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 93 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-674-008-5

Query Match 95.0%; Score 341; DB 1; Length 93;  
Best Local Similarity 97.0%; Pred. No. 2e-37;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KGVSLSPRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60  
1 |||||  
Db 22 KGVSLSPRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 81  
61 YLEKALN 67  
|||  
Db 82 YLEKALN 88

RESULT 5  
US-08-808-720-3  
Sequence 3, Application US/08808720  
Patent No. 6100387  
GENERAL INFORMATION:  
APPLICANT: Herrmann, Steve  
APPLICANT: Swandberg, Stephen  
TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING  
TITLE OF INVENTION: CHEMOKINE DOMAINS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark  
CITY: Cambridge  
STATE: MA  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/808,720  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Sprunger, Suzanne  
REGISTRATION NUMBER: P-41,323  
REFERENCE/DOCKET NUMBER: G15291  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8284  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 328 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-808-720-3

Query Match 95.0%; Score 341; DB 3; Length 326;  
Best Local Similarity 97.0%; Pred. No. 8.8e-37;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KGVSLSPRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60  
1 |||||  
Db 20 KGVSLSPRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 79  
61 YLEKALN 67  
|||  
Db 80 YLEKALN 86

RESULT 6  
US-08-808-720-1  
Sequence 1, Application US/08808720  
Patent No. 6100387  
GENERAL INFORMATION:  
APPLICANT: Herrmann, Steve  
APPLICANT: Swandberg, Stephen  
TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING  
TITLE OF INVENTION: CHEMOKINE DOMAINS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark  
CITY: Cambridge  
STATE: MA  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/808,720  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Sprunger, Suzanne  
REGISTRATION NUMBER: P-41,323  
REFERENCE/DOCKET NUMBER: G15291  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8284  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 328 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-808-720-1

Query Match 95.0%; Score 341; DB 3; Length 328;  
Best Local Similarity 97.0%; Pred. No. 8.8e-37;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KGVSLSPRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60  
1 |||||  
Db 22 KGVSLSPRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 81  
61 YLEKALN 67  
|||  
Db 82 YLEKALN 88

RESULT 7  
US-08-181-556-2  
Sequence 2, Application US/08181556  
Patent No. 5553486  
GENERAL INFORMATION:  
APPLICANT: HONJO, Tasuku  
APPLICANT: TASHIRO, Kei  
APPLICANT: TADA, Hideaki

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Query Match Similarity 94.7%; Score 340; DB 1; Length 89;
Best Local Similarity 95.5%; Pred. No. 2,5e-37;
Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0

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Db 22 KPVSLSPRCPCFFSFESHARAVKHLKIINTPCALQIVARLKNNRQVCIDPKLKWID 81
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OY 61 YLEKALN 67
    | | | | | |
Db 82 YLEKALN 88

RESULT 8
US-08-330-163-24
: Sequence 24, Application US/08330163
: Patent No. 5656724
: GENERAL INFORMATION:
: APPLICANT: Daly, Thomas J.
: APPLICANT: Larosa, Gregory J.
: TITLE OF INVENTION: Chemokine-Like Proteins and Methods of
: TITLE OF INVENTION: Use
: NUMBER OF SEQUENCES: 46
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: MA
: COUNTRY: U.S.A.
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.30B

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1  CURRENT APPLICATION DATA:
2  APPLICATION NUMBER:  US/08/330.163
3  FILING DATE:  05-AUG-1994
4  CLASSIFICATION:  530
5  ATTORNEY/AGENT INFORMATION:
6  NAME:  Fasse, J. Peter
7  REGISTRATION NUMBER:  32,983
8  REFERENCE/DOCKET NUMBER:  00231/080000
9  TELECOMMUNICATION INFORMATION:
10 TELEPHONE:  (617) 542-5070
11 TELEFAX:  (617) 542-8906
12 INFORMATION FOR SEQ ID NO:  24:
13
14 SEQUENCE CHARACTERISTICS:
15
16 LENGTH:  70 amino acids
17
18 TYPE:  amino acid
19
20 STRANDEDNESS:  single
21
22 TOPOLOGY:  linear
23
24 MOLECULE TYPE:  peptide
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26 US-08-330-163-24

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	Query Match	26.3%	Score 94.5;	DB 1	Length 70;	
	Best Local Similarity	32.8%;	Pred. No. 2.5e-05;			
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QY	 66 L 66   68 L 68					

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1      RESULT 9
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4      ; Patent No. 5789539
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Daly, Thomas J.
7      ; APPLICANT: Larosa, Gregory J.
8      ; TITLE OF INVENTION: Chemokine-Like Proteins and Methods of
9      ; TITLE OF INVENTION: Use
10     ; NUMBER OF SEQUENCES: 70
11     ; CORRESPONDENCE ADDRESS:
12     ; ADDRESSEE: Fish & Richardson P.C.
13     ; STREET: 225 Franklin Street
14     ; CITY: Boston
15     ; STATE: MA
16     ; COUNTRY: U.S.A.
17     ; ZIP: 02110-2804
18     ; COMPUTER READABLE FORM:
19     ; MEDIUM TYPE: Floppy disk
20     ; COMPUTER: IBM PC compatible
21     ; OPERATING SYSTEM: PC-DOS/MS-DOS
22     ; SOFTWARE: Patent In Release #1.0, Version #1.30B
23     ; CURRENT APPLICATION DATA:
24     ; APPLICATION NUMBER: US/08/482,111
25     ; FILING DATE: 07-JUN-1995
26     ; CLASSIFICATION: 514
27     ; ATTORNEY/AGENT INFORMATION:
28     ; NAME: Fasse, J. Peter
29     ; REGISTRATION NUMBER: 32,983
30     ; REFERENCE/DOCKET NUMBER: 00231/083001
31     ; TELECOMMUNICATION INFORMATION:
32     ; TELEPHONE: (617) 542-5070
33     ; TELEFAX: (617) 542-8906
34     ; INFORMATION FOR SEQ ID NO: 24:
35     ; SEQUENCE CHARACTERISTICS:
36     ; LENGTH: 70 amino acids
37     ; TYPE: amino acid
38     ; STRANDEDNESS: single
39     ; TOPOLOGY: linear
40     ; MOLECULE TYPE: peptide

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ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/244,702  
FILING DATE: 27-SEP-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/CA92/00528  
FILING DATE: 03-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,578  
FILING DATE: 04-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 8080-0004.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-244-702-9

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Best Local Similarity 32.3%; Pred. No. 2.8e-05;  
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

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DB 2 RCQCIKTYSKPFHPKFKEKLRIEISGPHCANTETIVKL-SDGRELCIDPKENMWQRYVER 60  
QY 65 AL 66  
DB 61 FL 62

RESULT 13  
US-08-244-702-10  
Sequence 10, Application US/08244702  
Patent No. 5665346  
GENERAL INFORMATION:  
APPLICANT: Clark-Lewis, Ian  
TITLE OF INVENTION: Human Interleukin-8 Analogs  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/244,702  
FILING DATE: 27-SEP-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/CA92/00528  
FILING DATE: 03-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,578

FILING DATE: 04-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 8080-0004.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-244-702-10

Query Match 26.2%; Score 94; DB 1; Length 68;  
Best Local Similarity 32.3%; Pred. No. 2.8e-05;  
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

QY 8 RCPC-REFESHVARANKHLIINT-PNCA-LQIVARLKNNNRQVCIDPKLWIOEYLEK 64  
DB 2 RCQCIKTYSKPFHPKFKEKLRIEISGPHCANTETIVKL-SDGRELCIDPKENMWQRYVER 60  
QY 65 AL 66  
DB 61 FL 62

RESULT 14  
US-08-244-702-11  
Sequence 11, Application US/08244702  
Patent No. 5665346  
GENERAL INFORMATION:  
APPLICANT: Clark-Lewis, Ian  
TITLE OF INVENTION: Human Interleukin-8 Analogs  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 2000 Pennsylvania Avenue, N.W., Suite 5500  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/244,702  
FILING DATE: 27-SEP-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/CA92/00528  
FILING DATE: 03-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,578  
FILING DATE: 04-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 8080-0004.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 68 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-244-702-11







GenCore version 5.1.3  
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(without alignments)  
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Title: US-09-852-424-4

Perfect score: 359

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Maximum Match 100%

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	344	95.8	67	9	US-09-852-424-3
6	344	95.8	67	9	US-09-852-424-6
7	343	95.5	67	9	US-09-852-424-9
8	342	95.3	67	9	US-09-852-424-2
9	342	95.3	67	9	US-09-852-424-5
10	341	95.0	67	9	US-09-835-107-1
11	341	95.0	67	10	US-09-144-838-8
12	341	95.0	67	10	US-09-144-838-23
13	341	95.0	89	8	US-08-927-939-22
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15	341	95.0	89	10	US-09-953-682-4
16	341	95.0	89	10	US-09-953-717-4
17	341	95.0	93	8	US-08-927-939-56
18	341	95.0	93	9	US-09-835-107-2
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22	341	95.0	93	10	US-09-919-497-95	Sequence 95, Appl
23	341	95.0	320	9	US-09-792-793A-77	Sequence 77, Appl
24	341	95.0	322	9	US-09-792-793A-78	Sequence 78, Appl
25	341	95.0	327	9	US-09-792-793A-79	Sequence 79, Appl
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28	330.5	92.1	66	9	US-09-852-424-10	Sequence 10, Appl
29	323.5	90.1	66	10	US-09-144-838-27	Sequence 27, Appl
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31	304	84.7	67	10	US-09-144-838-52	Sequence 52, Appl
32	290	80.8	68	10	US-09-144-838-24	Sequence 24, Appl
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42	218	60.7	67	10	US-09-144-838-31	Sequence 31, Appl
43	215	59.9	69	10	US-09-144-838-54	Sequence 54, Appl
44	207.5	57.8	66	10	US-09-144-838-35	Sequence 35, Appl
45	199	55.4	68	10	US-09-144-838-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1

US-09-852-424-4

; Sequence 4, Application US/09852424

; Patent No. US20020156034A1

GENERAL INFORMATION:

APPLICANT: The University of British Columbia; and

APPLICANT: Chemokine Therapeutics Corporation

TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS

FILE REFERENCE: 80021-257

CURRENT APPLICATION NUMBER: US/09/852,424

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: CA 2,305,787

PRIOR FILING DATE: 2000-05-09

PRIOR APPLICATION NUMBER: US 60/205,467

PRIOR FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 135

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4

LENGTH: 67

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Engineered in

US-09-852-424-4

Query Match

Best Local Similarity 100.0%; Score 359; DB 9; Length 67;

Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGVSLSPRCPCRFESHVARANKYKILITPICALQIVARLKNNNROYCIDPKLKWIOE 60

Db 1 KGVSLSPRCPCRFESHVARANKYKILITPICALQIVARLKNNNROYCIDPKLKWIOE 60

QY 61 YLEKALN 67

Db 61 YLEKALN 67

RESULT 2

US-09-852-424-8

; Sequence 8, Application US/09852424

```
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 67
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (7)
; OTHER INFORMATION: Xaa-P*-proline-amino acid chimera. See page 17 of
; OTHER INFORMATION: disclosure for possible structures for P*
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-8
```

```
Query Match          97.5%; Score 350; DB 9; Length 67;
Best Local Similarity 98.5%; Pred. No. 2,1e-32;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 KGVSLSPRCRPFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
Db      1 KGVSLSPRCRPFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
```

```
OY      61 YLEKALN 67
Db      61 YLEKALN 67
```

```
RESULT 3
US-09-852-424-1
; Sequence 1, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 67
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-1
```

```
Query Match          97.2%; Score 349; DB 9; Length 67;
Best Local Similarity 98.5%; Pred. No. 2,7e-32;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 KGVSLSPRCRPFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
Db      1 KGVSLSPRCRPFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
```

```
OY      61 YLEKALN 67
Db      61 YLEKALN 67
```

```
RESULT 4
US-09-852-424-7
; Sequence 7, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 67
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (6)
; OTHER INFORMATION: Xaa-P*-proline-amino acid chimera. See page 17 of
; OTHER INFORMATION: disclosure for possible structures for P*
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-7
```

```
Query Match          96.1%; Score 345; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 7,5e-32;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      1 KGVSLSPRCRPFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
Db      1 KGVSLSPRCRPFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY      61 YLEKALN 67
Db      61 YLEKALN 67
```

```
RESULT 5
US-09-852-424-3
; Sequence 3, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 67
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
```

US-09-852-424-3

Query Match	95.88;	Score 344;	DB 9;	Length 67;
Best Local Similarity	97.08;	Pred. NO. 9.7e-32;		
Matches 65; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 1 KGVSLSPRCRCRFEEHVARAVYKHLKLTNPNCALQIVARLKNNRQVCIDPKLKIQE 60  
|||||  
Db 1 KGVSLPYRCRCRFEEHVARAVYKHLKLTNPNCALQIVARLKNNRQVCIDPKLKIQE 60

Qy	61	YLEKALN	67
Db	61	YLEKALN	67

RESULT 6  
US-09-852-424-6  
: Sequence 6, Application US/09852424  
: Patent No. US20090156024A1

1 APPLICANT: The University of British Columbia; and  
 2 APPLICANT: Chemokine Therapeutics Corporation  
 3 TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
 4 FILE REFERENCE: 80021-257  
 5 CURRENT APPLICATION NUMBER: US/09/852,424  
 6 CURRENT FILING DATE: 2001-09-26  
 7 PRIOR APPLICATION NUMBER: CA 2,305,787  
 8 PRIOR FILING DATE: 2000-05-09  
 9 PRIOR APPLICATION NUMBER: US 60/205,467  
 10 PRIOR FILING DATE: 2000-05-19  
 11 NUMBER OF SEQ ID NOS: 135  
 12 SOFTWARE: PatentIn Ver. 2.0  
 13  
 14 SEQ ID NO: 6  
 15 LENGTH: 67  
 16 TYPE: PRT  
 17 ORGANISM: Artificial Sequence  
 18 FEATURE:  
 19 NAME/KEY: MUTAGEN  
 20 LOCATION: (5)  
 21 OTHER INFORMATION: Xaa=P\*proline-amino acid chimera. See page 17 of  
 22 OTHER INFORMATION: disclosure for possible structures for P\*  
 23 OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
 24 IS-09-852-424-6 Laboratory

Query Match	95.8%;	Score 344;	DB 9;	Length 67;
Best Local Similarity	97.0%;	Pred. NO. 9.7e-32;		
Matches 65; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy 1 KGVSLSPPCRPFEEHVARAVKHLKLTNPNCALQIVARLKNNRQVCIDPKLWIOE 600  
|||||  
Db 1 KGVSVSYRCRPFEEHVARAVKHLKLTNPNCALQIVARLKNNRQVCIDPKLWIOE 600

Qy	61 YLEKALN 67
Db	61 YLEKALN 67

RESULT 7  
US-09-852-424-9  
; Sequence 9, Application US/09852424  
; Patent No. US20020156034A1

1 APPLICANT: The University of British Columbia, and  
 2 APPLICANT: Chemokine Therapeutics Corporation  
 3 TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
 4 FILE REFERENCE: 80021-257  
 5 CURRENT APPLICATION NUMBER: US/09/852,424  
 6 CURRENT FILING DATE: 2001-09-26  
 7 PRIOR APPLICATION NUMBER: CA 2,305,787  
 8 PRIOR FILING DATE: 2000-05-09  
 9 PRIOR APPLICATION NUMBER: US 60/205,467  
 10 PRIOR FILING DATE: 2000-05-19

```

; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9

```

```

; OTHER INFORMATION: Xaa=P*-proline-amino acid chimera. See page 17 ob
; OTHER INFORMATION: disclosure for possible structures for P*
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-9

```

Query Match	95.5%	Score 343	DB 9	Length 67
Best Local Similarity	97.0%	Pred. No. 1.3e-31		
Matches 65	Conservative	0	Mismatches 2	Indels 0
				Gaps 0

QY	61	YLEKALN	67
Db	61	YLEKALN	67

RESULT 8  
US-09-852-424-2  
; Sequence 2, Application US/09852422  
; Patent No. US20020156034A1

```

: APPLICANT: The University of British Columbia, and
: APPLICANT: Chemokine Therapeutics Corporation
: TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
: FILE REFERENCE: 80021-257
: CURRENT APPLICATION NUMBER: US/09/852,424
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: CA 2,305,787
: PRIOR FILING DATE: 2000-05-09
: PRIOR APPLICATION NUMBER: US 60/205,467
: PRIOR FILING DATE: 2000-05-19
: NUMBER OF SEQ ID NOS: 135
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 67
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Engineered In
: OTHER INFORMATION: Laboratory
: US-09-852-424-2

```

Query Match	95.3%;	Score 342;	DB 9;	Length 67;
Best Local Similarity	97.0%;	Pred. No. 1.6e-31;		
Matches 65;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 1 KGVSLSPRCRCRFESHVARANVKHLINTPNCALQIVARLKNNNRQVCIDPKLWIOE 600  
|||||  
Db 1 KGVSPSYRCRCRFESHVARANVKHLINTPNCALQIVARLKNNNRQVCIDPKLWIOE 600

QY	61 YLEKALN 67
Db	61 YLEKALN 67

RESULT 9  
US-09-852-424-5  
; Sequence 5; Application US/09852424  
; Patent No. US30020156034A1  
; GENERAL INFORMATION:  
; APPLICANT: The University of British Columbia; and

```
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
US-09-852-424-5
```

```
Query Match          95.3%; Score 342; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 1,6e-31;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 KGVSLSPRCPCRFESHVARANKHLKILNTPNCALQIYARLKNNNROVCIDPKLKWIOE 60
    |||||
DB 1 KGVSLSPRCPCRFESHVARANKHLKILNTPNCALQIYARLKNNNROVCIDPKLKWIOE 60
```

```
QY 61 YLEKALN 67
    |||||
DB 61 YLEKALN 67
```

```
RESULT 10
US-09-835-107-1
; Sequence 1, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhder
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Johanne
; APPLICANT: Clark-Lewis
; APPLICANT: Salari, Hassan
; TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: SMAR012
; CURRENT APPLICATION NUMBER: US/09/835,107
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: CA 2,305,036
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/222,425
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: CA 2,335,109
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SDF-1 alpha
US-09-835-107-1
```

```
Query Match          95.0%; Score 341; DB 9; Length 67;
Best Local Similarity 97.0%; Pred. No. 2,1e-31;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 KGVSLSPRCPCRFESHVARANKHLKILNTPNCALQIYARLKNNNROVCIDPKLKWIOE 60
    |||||
DB 1 KPVSLSPRCPCRFESHVARANKHLKILNTPNCALQIYARLKNNNROVCIDPKLKWIOE 60
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```
QY 61 YLEKALN 67
    |||||
DB 61 YLEKALN 67
```

```
RESULT 11
US-09-144-838-8
; Sequence 8, Application US/09144838A
; Patent No. US20020051996A1
; GENERAL INFORMATION:
; APPLICANT: Siani, Michael A.
; APPLICANT: Wilken, Jill
; APPLICANT: Simon, Reyna
; APPLICANT: Kent, Stephen B.H.
; TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
; FILE REFERENCE: GREN-020/01US
; CURRENT APPLICATION NUMBER: US/09/144,838A
; CURRENT FILING DATE: 1998-08-31
; EARLIER APPLICATION NUMBER: US 60/057,620
; EARLIER FILING DATE: 1997-09-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 8
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-144-838-8
```

```
Query Match          95.0%; Score 341; DB 10; Length 67;
Best Local Similarity 97.0%; Pred. No. 2,1e-31;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 KGVSLSPRCPCRFESHVARANKHLKILNTPNCALQIYARLKNNNROVCIDPKLKWIOE 60
    |||||
DB 1 KPVSLSPRCPCRFESHVARANKHLKILNTPNCALQIYARLKNNNROVCIDPKLKWIOE 60
```

```
QY 61 YLEKALN 67
    |||||
DB 61 YLEKALN 67
```

```
RESULT 12
US-09-144-838-23
; Sequence 23, Application US/09144838A
; Patent No. US20020051996A1
; GENERAL INFORMATION:
; APPLICANT: Siani, Michael A.
; APPLICANT: Wilken, Jill
; APPLICANT: Simon, Reyna
; APPLICANT: Kent, Stephen B.H.
; TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
; FILE REFERENCE: GREN-020/01US
; CURRENT APPLICATION NUMBER: US/09/144,838A
; CURRENT FILING DATE: 1998-08-31
; EARLIER APPLICATION NUMBER: US 60/057,620
; EARLIER FILING DATE: 1997-09-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 23
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-144-838-23
```

```
Query Match          95.0%; Score 341; DB 10; Length 67;
Best Local Similarity 97.0%; Pred. No. 2,1e-31;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Search completed: January 23, 2003, 15:38:01  
Job time : 6.2 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:31:02 : Search time 11.6 Seconds

(without alignments)  
555.259 Million cell updates/sec

Title: US-09-852-424-4

Perfect score: 359

Sequence: 1 KGVSLSPRCPCRFESHVAR.....QVCIDPKLKWIEYLEKALN 67

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR\_73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	341	95.0	93	2	G01540
2	340	94.7	89	2	A53497
3	340	94.7	89	2	I53416
4	340	94.7	93	2	I81182
5	101	28.1	101	2	I48148
6	96	26.7	95	2	JN0841
7	94	26.2	99	2	A37034
8	94	26.2	120	2	I48147
9	91.5	25.5	91	1	A46539
10	91.5	25.5	96	2	A32954
11	91	25.3	103	2	S42496
12	90	25.1	103	2	A53096
13	87.5	24.4	96	2	JN0572
14	87	24.2	101	2	I46871
15	86.5	24.1	91	1	A28815
16	86	24.0	109	2	A54678
17	83.5	23.3	100	2	JH0200
18	82.5	23.0	75	2	A54188
19	82	22.8	120	2	JE0177
20	81.5	22.7	75	2	B54188
21	81.5	22.7	119	2	I52322
22	81.5	22.7	119	2	S42881
23	80	22.3	148	1	A30209
24	80	22.3	148	1	S07723
25	79.5	22.1	107	2	B38290
26	78.5	21.9	100	2	S21467
27	78.5	21.9	100	2	I55614
28	78.5	21.9	132	2	A57325
29	77.5	21.6	101	2	B28414

30	77.5	21.6	107	2	A28414	melanoma growth-st
31	77.5	21.6	114	2	A55010	neutrophil-activat
32	77.5	21.6	117	2	B44253	alveolar macrophag
33	76.5	21.3	103	2	A28736	transformation-ind
34	76.5	21.3	103	2	I50417	RSV-induced protei
35	74.5	20.8	96	2	I48099	ectaxin precursor
36	74	20.6	92	2	A32393	macrophage inflamm
37	73.5	20.5	107	2	JH0281	macrophage inflamm
38	73.5	20.5	870	2	A41130	dystrophin homolog
39	72.5	20.2	126	2	A35766	platelet factor 4,
40	72	20.1	96	2	JC2478	ectaxin precursor
41	71.5	19.9	92	2	I46730	immune activation
42	71.5	19.9	128	1	TGHU	beta-thromboglobul
43	70.5	19.6	53	2	I64831	gene KC protein -
44	69.5	19.4	104	1	PRHUA	platelet factor 4
45	69	19.2	93	2	B35673	LD78-beta protein

#### ALIGNMENTS

```
RESULT 1
G01540
cytokine SDF-1-beta - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 26-Aug-1999
C:Accession: G01540
R:Spocila, L.D.
submitted to the EMBL Data Library, October 1994
A:Reference number: G07697
A:Accession: G01540
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-93 <SPO>
A:Cross-References: EMBL:016752; NID:q1272194; PID:9571508
C:Superfamily: beta-thromboglobulin

Query Match
Best Local Similarity 95.0% Score 341; DB 2; Length 93;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 KGVSLSPRCPCRFESHVARANKHLKLNTPNCALQIVARLKNNNRQVCIDPKLKWIE 60
Db 22 KGVSLSPRCPCRFESHVARANKHLKLNTPNCALQIVARLKNNNRQVCIDPKLKWIE 81
Oy 61 YLEKALN 67
Db 82 YLEKALN 88

RESULT 2
A53497
pre-B-cell growth-stimulating factor precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 20-Jun-2000
C:Accession: A53497; I59582
R:Nagasawa, T.; Kikutani, H.; Kishimoto, T.
Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994
A:Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.
A:Reference number: A53497; MUID:94181581; PMID:8134392
A:Accession: A53497
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-89 <NAG>
A:Cross-References: GB:D21072; NID:9413905; PID:BA04648.1; PID:9468457
R:Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993
A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I me
A:Reference number: I59582; MUID:93342488; PMID:8342023
A:Accession: I59582
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89 <RSS>
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RESULT 7  
A37034  
Interleukin-8 precursor - human  
N:Alternate names: beta-thromboglobulin-like protein; fibroblast-derived neutrophil-activating factor  
C:Species: Homo sapiens (nan)  
C:Date: 08-Dec-1992 #sequence, revision 08-Dec-1992 #text, change 20-Aug-1999  
C:Accession: A37034; J05041; A32791; S37634; P10107; A28598; A27488; A39960; A60401; A60402  
R:Murakami, N.; Shiroo, M.; Matsushima, K.  
J. Immunol. 143, 1366-1371, 1989  
A:Title: Genomic structure of the human monocyte-derived neutrophil chemotactic factor I  
A:Reference number: A37034; MUID:89309826; PMID:2663993  
A:Accession: A37034  
A:Molecule type: DNA  
A:Residues: 1-99 <DNA>  
A:Cross-references: GB:M28130; NID:9186367; PIDN:AAA59158.1; PID:9186368  
A:Note: The authors failed to translate the last thirty-six nucleotides of the second ex R:Matsushima, K.; Morishita, K.; Yoshimura, T.; Lavu, S.; Kobayashi, Y.; Lew, W.; Appella, J. Exp. Med. 167, 1883-1893, 1988  
A:Title: Molecular cloning of a human monocyte-derived neutrophil chemotactic factor (M A:Reference number: J10041; MUID:88258376; PMID:3260265  
A:Accession: J10041  
A:Molecule type: mRNA  
A:Residues: 1-99 <MA1>  
A:Cross-references: EMBL:Y00787; NID:934518; PIDN:CAA68742.1; PID:934519  
A:Note: the sequence shows similarity to several platelet-derived factors, a v-src-induced R:Kowalski, J.; Denhardt, D.T.  
Mol. Cell. Biol. 9, 1946-1957, 1989  
A:Title: Regulation of the mRNA for monocyte-derived neutrophil-activating peptide in d A:Reference number: A37791; MUID:89313739; PMID:2664463  
A:Accession: A37791  
A:Molecule type: mRNA  
A:Residues: 1-99 <KOW>  
A:Cross-references: GB:M25383; NID:9188627; PIDN:AAA6323.1; PID:9188628  
R:King, C.H.; Gordon, G.S.; Konieczkowski, M.; Sedot, J.R.  
Submitted to the EMBL Data Library, February 1992  
A:Reference number: S37634  
A:Accession: S37634  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-97 <KIN>  
A:Cross-references: EMBL:Z11886; NID:933958; PIDN:CAA7745.1; PID:933959  
R:Suzuki, K.; Miyasaka, H.; Ota, H.; Yamakawa, Y.; Tagawa, M.; Kuramoto, A.; Mizuno, S. J. Exp. Med. 169, 1895-1901, 1989  
A:Title: Purification and partial primary sequence of a chemotactic protein for polymorph A:Reference number: P10107; MUID:89279141; PMID:2659722  
A:Accession: P10107  
A:Molecule type: protein  
A:Residues: 23-32, 'X', '35', 'X', '37-52', 'L', '54' <SU2>  
A:Experimental source: lung giant cell carcinoma LU65C  
R:Gregory, H.; Young, J.; Schroeder, J.M.; Mrowietz, U.; Christophers, E.  
Blochem. Biophys. Res. Commun. 151, 883-890, 1988  
A:Title: Structure determination of a human lymphocyte derived neutrophil activating pep A:Reference number: A28598; MUID:88162914; PMID:3279957  
A:Accession: A28598  
A:Molecule type: protein  
A:Residues: 28-99 <GRB>  
R:Walt, A.; Peverl, P.; Aschauer, H.; Baggiolini, M.  
Blochem. Biophys. Res. Commun. 149, 755-761, 1987  
A:Title: Purification and amino acid sequencing of NAF, a novel neutrophil-activating fa A:Reference number: A27488; MUID:88106502; PMID:3322281  
A:Accession: A27488  
A:Molecule type: protein  
A:Residues: 28-59 <MAL>  
R:Yoshimura, T.; Matsushima, K.; Tanaka, S.; Robinson, E.A.; Appella, E.; Oppenheim, J.J. Proc. Natl. Acad. Sci. U.S.A. 84, 9233-9237, 1987  
A:Title: Purification of a human monocyte-derived neutrophil chemotactic factor that has A:Reference number: A39960; MUID:88097462; PMID:3480540  
A:Accession: A39960  
A:Molecule type: protein  
A:Residues: 28-69 <YOS>  
R:Schroeder, J.M.; Sticherling, M.; Hennelcke, H.H.; Preissner, W.C.; Christophers, E. J. Immunol. 144, 2223-2232, 1990

A:Title: IL-1alpha or tumor necrosis factor-alpha stimulate release of three NAF-1/II A:Reference number: A60401; MUID:90187866; PMID:2179408  
A:Accession: A60401  
A:Molecule type: protein  
A:Residues: 23-32 <SCH>  
A:Experimental source: dermal fibroblasts  
A:Note: a minor component of this material (15%) includes an additional two amino aci R:Van Damme, J.; Decock, B.; Conings, R.; Lemeers, J.P.; Odenacker, G.; Billiau, A. Eur. J. Immunol. 19, 1189-1194, 1989  
A:Title: The chemotactic activity for granulocytes produced by virally infected fibro A:Reference number: A60591; MUID:89338542; PMID:2668011  
A:Accession: A60591  
A:Molecule type: protein  
A:Residues: 23-33, 'X', '35', 'X', '37-42' <VAN>  
R:Nakagawa, H.; Hatakeyama, S.; Ikesue, A.; Miyai, H. FEBS Lett. 282, 412-414, 1991  
A:Title: Generation of interleukin-8 by plasmin from AVPR-interleukin-8, the human f A:Reference number: S15827; MUID:91243843; PMID:1828038  
A:Accession: S15827  
A:Molecule type: protein  
A:Residues: 23-33, 'X', '35', 'X', '37-47' <FEB>  
R:Van Damme, J.; Van Beeumen, J.; Conings, R.; Decock, B.; Billiau, A. Eur. J. Biochem. 181, 337-344, 1989  
A:Title: Purification of granulocyte chemotactic peptide/interleukin-8 reveals N-term A:Reference number: S04216; MUID:89231715; PMID:2523801  
A:Accession: S04216  
A:Molecule type: protein  
A:Residues: 21-67 <VAN>  
R:Yoshimura, T.; Robinson, E.A.; Appella, E.; Matsushima, K.; Showalter, S.D.; Skeel, M.O. Immunol. 26, 87-93, 1989  
A:Title: Three forms of monocyte-derived neutrophil chemotactic factor (MNCFC) distri A:Reference number: A60567; MUID:89181532; PMID:2648135  
A:Accession: A60567  
A:Molecule type: protein  
A:Residues: 21-33, 'X', '35', 'X', '37-47' <YOS>  
A:Note: the forms starting from positions 21, 23, and 28 represented 8%, 47%, and 45% R:Van Damme, J.; Van Beeumen, J.; Odenacker, G.; Billiau, A. J. Exp. Med. 167, 1364-1376, 1988  
A:Title: A novel, NH-2-terminal sequence-characterized human monokine possessing neut A:Reference number: A60847; MUID:88187604; PMID:3258625  
A:Accession: A60847  
A:Molecule type: protein  
A:Residues: 28-47 <VAB>  
R:Car, B.D.; Baggiolini, M.; Walz, A. Blochem. J. 275, 581-584, 1991  
A:Title: Formation of neutrophil-activating peptide 2 from platelet-derived connectiv A:Reference number: S15417; MUID:91248085; PMID:2039437  
A:Accession: S15417  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 28-99 <CAR>  
R:Golds, E.E.; Mason, P.; Nyirkos, P. Blochem. J. 259, 585-588, 1989  
A:Title: Inflammatory cytokines induce synthesis and secretion of gro protein and a n A:Reference number: S03975; MUID:89246368; PMID:2655853  
A:Accession: S03975  
A:Molecule type: protein  
A:Residues: 23-46 <GOL>  
R:Hotta, K.; Hayashi, K.; Ishikawa, J.; Tagawa, M.; Hashimoto, K.; Mizuno, S.; Suzuki Immunol. Lett. 24, 165-170, 1990  
A:Title: Coding region structure of interleukin-8 gene of human lung giant cell carci A:Reference number: I54560; MUID:90346419; PMID:2200751  
A:Accession: I54560  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-99 <DNA>  
A:Cross-references: GB:D14283; NID:9219915; PIDN:BA03245.1; PID:9219916  
R:Schmid, J.; Weissmann, C. Eur. J. Immunol. 139, 250-256, 1987  
A:Title: Induction of mRNA for a serine protease and a beta-thromboglobulin-like prot A:Reference number: I55992; MUID:87224164; PMID:2953813  
A:Accession: I55992  
A:Status: preliminary; translated from GB/EMBL/DBJ



R:Quendo, P.; Alberta, J.; Wen, D.; Graycar, J.L.; Derynck, R.; Stiles, C.D.  
 J. Biol. Chem. 264, 4133-4137, 1989  
 A:Title: Chem. 264, 4133-4137, 1989  
 A:Reference number: A32954; MUID:89139485; PMID:2917992  
 A:Accession: A32954  
 A:Molecule type: mRNA  
 A:Residues: 1-96 <COU>  
 A:Cross-references: GB:J04596; NID:9201042; PIDN:AAA40131.1; PID:9201043  
 R:Ryseck, R.P.; Macdonald-Bravo, H.; Matzel, M.G.; Bravo, R.  
 Exp. Cell. Res. 180, 266-275, 1989  
 A:Title: Cloning and sequence of a secretory protein induced by growth factors in mouse  
 A:Reference number: JH0081; MUID:89078502; PMID:2909392  
 A:Accession: JH0081  
 A:Molecule type: mRNA  
 A:Residues: 1-96 <RVS>  
 C:Comment: This protein is basic and lacks threonine, phenylalanine, and tyrosine.  
 C:Genetics: 5  
 A:Map position: 5  
 C:Superfamily: beta-thromboglobulin  
 C:Keywords: extracellular protein  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-96/Product: gro-alpha #status predicted <MAT>

Query Match 25.5%; Score 91.5; DB 2; Length 96;  
 Best Local Similarity 32.8%; Pred. No. 0.00047;  
 Matches 20; Conservative 17; Mismatches 21; Indels 3; Gaps 3;

Oy 8 RCPREFESHVARANVHKIL-LTPNCA-LQIYARLKNRRQVCIDPKLMOEYLEKA 65  
 Db 32 RCOCLQTMAGIHLKNISLKVLPSCPTQTEVIATLK-NGREACLDPEALVOKIVQKM 90  
 Oy 66 L 66  
 Db 91 L 91

# RESULT 11

S42496

Interleukin-8 precursor [similarity] - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 19-Jan-2001  
 C:Accession: S42496; I46997  
 R:Legasteleis, I.; Greenland, T.; Arnaud, P.; Mornex, J.F.; Cordier, G.  
 Submitted to the EMBL Data Library, March 1994  
 A:Description: Nucleotide sequence of ovine Interleukin 8 cDNA using polymerase chain re  
 A:Reference number: S42496  
 A:Accession: S42496  
 A:Molecule type: mRNA  
 A:Residues: 1-101 <LEG>  
 A:Cross-references: EMBL:X78306; NID:9463253; PIDN:CAA55115.1; PID:9463254  
 R:Scow, H.F.; Yoshimura, T.; Wood, P.R.; Colditz, I.G.  
 Immunol. Cell Biol. 72, 398-405, 1994  
 A:Title: Cloning, sequencing, expression and inflammatory activity in skin of ovine inte  
 A:Reference number: I46997; MUID:95137691; PMID:7835984  
 A:Accession: I46997  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-101 <SEO>  
 A:Cross-references: GB:S74436; NID:9786590; PIDN:AA83241.1; PID:9786591  
 C:Genetics: 8  
 A:Gene: IL-8  
 C:Superfamily: beta-thromboglobulin  
 C:Keywords: chemotaxis, cytokine, inflammation  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-101/Product: Interleukin-8 #status predicted <MAT>

Query Match 25.3%; Score 91; DB 2; Length 101;  
 Best Local Similarity 30.4%; Pred. No. 0.00057;  
 Matches 21; Conservative 20; Mismatches 20; Indels 8; Gaps 5;

Oy 3 VSLSPRCRPFESHVARAN--VKHLKILMT-PNCA-LQIYARLKNRRQVCIDPKLKW 57  
 Db 28 MSTELRCQ--IKTHSTFPHKFIKELRVIESGPCENSEIIVKL-TNGKEVCIDPKKEK 84

Oy 58 IOEYLEKAL 66  
 Db 85 VQKVWQ 93

# RESULT 12

A53096

Interleukin-8 precursor - pig

N:Alternate names: alveolar macrophage chemotactic factor-I (AMCF-I)  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 02-Jun-1995 #sequence\_revision 02-Jun-1995 #text\_change 19-Jan-2001  
 C:Accession: A53096; A44253  
 R:Lin, G.; Pearson, A.E.; Scamurra, R.W.; Zhou, Y.; Baarsch, M.J.; Weiss, D.J.; Murta  
 J. Biol. Chem. 269, 77-85, 1994  
 A:Title: Regulation of Interleukin-8 expression in porcine alveolar macrophages by ba  
 A:Reference number: A53096; MUID:94103307; PMID:8276881  
 A:Accession: A53096  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-103 <LIN>  
 A:Cross-references: GB:M86923; NID:9164520; PIDN:AAA1616.1; PID:9164521  
 R:Goodman, R.B.; Foster, D.C.; Mathews, S.L.; Osborn, S.G.; Kuijper, J.L.; Forstrom,  
 Biochemistry 31, 10483-10490, 1992  
 A:Title: Molecular cloning of porcine alveolar macrophage-derived neutrophil chemotac  
 A:Reference number: A44253; MUID:93041741; PMID:1420165  
 A:Accession: A44253  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-22, 'D', 24-103 <GOO>  
 A:Cross-references: GB:M99367; NID:91235611  
 A:Experimental source: alveolar macrophage  
 A>Note: sequence extracted from NCBI backbone (NCBI:117415, NCBI:117416)  
 A:Note: the sequence in Genbank entry PIGAMCT, release 117.0, has been corrected to  
 C:Superfamily: beta-thromboglobulin  
 C:Keywords: chemotaxis; cytokine; inflammation  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-103/Product: Interleukin-8 #status predicted <MAT>

Query Match 25.1%; Score 90; DB 2; Length 103;  
 Best Local Similarity 31.8%; Pred. No. 0.00077;  
 Matches 21; Conservative 18; Mismatches 19; Indels 8; Gaps 5;

Oy 3 VSLSPRCRPFESHVARAN--VKHLKILMT-PNCA-LQIYARLKNRRQVCIDPKLKW 57  
 Db 28 VSAELRCQ--IKTHSTFPHKFIKELRVIESGPCENSEIIVKL-VNGKEVCIDPKKEK 84

Oy 58 IOEYLE 63  
 Db 85 VQKVWQ 90

# RESULT 13

JN0572

neutrophil chemo-attractant gro protein precursor - rat

N:Alternate names: CINC: cytokine-induced neutrophil chemoattractant; Interleukin-8-1  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 20-Jun-2000  
 C:Accession: JN0572; JQ1519; A34481; A48988; B48988; S51214  
 R:Knishl, K.; Takata, Y.; Yamamoto, M.; Yomogida, K.; Watanabe, K.; Tsurufuji, S.; F  
 Gene 126, 285-286, 1993  
 A:Title: Structure of the gene encoding rat neutrophil chemo-attractant Gro.  
 A:Reference number: JN0572; MUID:93246259; PMID:8462545  
 A:Accession: JN0572  
 A:Molecule type: DNA  
 A:Residues: 1-96 <KON>  
 A:Cross-references: DBJ:D11445; NID:9391854; PIDN:BA02009.1; PID:9220755  
 R:Hang, S.; Paulauskis, J.D.; Kobzik, L.  
 Biochem. Biophys. Res. Commun. 184, 922-929, 1992  
 A:Title: Rat KC cDNA cloning and mRNA expression in lung macrophages and fibroblasts.  
 A:Reference number: JQ1519; MUID:92246987; PMID:1374243  
 A:Accession: JQ1519  
 A:Molecule type: mRNA



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 23, 2003, 15:28:07 : Search time 6 seconds

(without alignments)  
463.152 Million cell updates/sec

Title: US-09-852-424-4  
Sequence: 1 KGVSLSPRCRCRPFESHVAR.....QVCIDPKLKMIGEVLEKALN 67

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SWISSPROT\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	341	95.0	93	1	SDF1_FELCA
2	341	95.0	93	1	SDF1_HUMAN
3	340	94.7	89	1	SDF1_MOUSE
4	101	28.1	101	1	IL8_CAVPO
5	99	27.6	101	1	IL8_CANFA
6	96	26.7	101	1	IL8_FELCA
7	94	26.2	99	1	IL8_HUMAN
8	94	26.2	120	1	SY02_CAVPO
9	91.5	25.5	91	1	SY05_MOUSE
10	91.5	25.5	92	1	SY05_RAT
11	91.5	25.5	96	1	GRO_MOUSE
12	91	25.3	101	1	IL8_MACMU
13	91	25.3	101	1	IL8_SHEEP
14	90	25.1	103	1	IL8_PIG
15	88.5	24.7	91	1	SY05_CAVPO
16	88	24.5	101	1	IL8_BOVIN
17	88	24.5	130	1	SY05_RAT
18	87.5	24.4	96	1	GRO_RAT
19	87	24.2	101	1	IL8_CERTO
20	87	24.2	101	1	IL8_RABIT
21	86.5	24.1	91	1	SY05_HUMAN
22	86	24.0	99	1	SY07_HUMAN
23	85.5	23.8	50	1	SY05_PIG
24	83.5	23.3	100	1	MIP2_MOUSE
25	82.5	23.0	114	1	SY06_HUMAN
26	81.5	22.7	71	1	GRO1_HUMAN
27	81.5	22.7	92	1	SY03_RAT
28	81.5	22.7	112	1	SY06_BOVIN
29	81.5	22.7	119	1	SY07_PIG
30	81	22.6	120	1	SY16_HUMAN
31	80	22.3	148	1	SY02_MOUSE
32	80	22.3	148	1	SY02_RAT
33	79.5	22.1	91	1	SY05_BOVIN

34	79.5	22.1	107	1	M12B_HUMAN	P19876 homo sapien
35	79	22.0	89	1	SY18_HUMAN	P55774 h small ind
36	79	22.0	98	1	SY14_HUMAN	O99616 homo sapien
37	79	22.0	119	1	SY24_MOUSE	O91K60 mus musculus
38	78.5	21.9	100	1	MIP2_RAT	P30348 ratius norv
39	78.5	21.9	132	1	SY05_MOUSE	P50228 mus musculus
40	78	21.7	97	1	SY08_MOUSE	O94121 mus musculus
41	78	21.7	109	1	SY13_HUMAN	O43927 homo sapien
42	77.5	21.6	101	1	GRO_CHICK	P09340 cricetus
43	77.5	21.6	107	1	GRO_HUMAN	P09341 homo sapien
44	77.5	21.6	114	1	SY05_HUMAN	P42830 homo sapien
45	77.5	21.6	117	1	AMC2_PIG	P22952 sus scrofa

## ALIGNMENTS

## RESULT 1

SDF1\_FELCA  
ID SDF1\_FELCA STANDARD: PRT: 93 AA.

AC 062657: FELCA

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12).

GN SDF1.

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OX NCBI\_TaxID=9685;

RE [1]

SEQUENCE FROM N.A.

RC TISSUE=Thymus;

RX MEDLINE=98450506; PubMed=9777331;

RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K.,

RA Cai J.S., Sato E., Kohmoto M., Mikami T.;

RT "Molecular cloning and sequencing of feline stromal cell-derived

RT factor-1 alpha and beta."

RL Eur. J. Immunogenet. 23:303-305(1998).

CC -! FUNCTION: CHEMOKINE RECEPTOR ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT

CC NOT NEUTROPHILS.

CC -! ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA AND BETA (SHOWN HERE);

CC ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -! SIMILARITY: BELONGS TO THE INTERKINE ALPHA FAMILY (SMALL CYTOKINE

CC C-X-C) (CHEMOKINE CXC).

CC -----

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CC -----

CC EMBL: AB011966; BAA28602.1; -

DR HSP: P48061; ISDP.

DR InterPro: IPR001089; CXC\_chim\_kine\_sm1.

DR InterPro: IPR001811; Chemokine\_IL8.

DR Pfam: PF00048; IL8; 1.

DR SMART: SM00199; SCY; 1.

DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; FALSE\_NEG.

KW Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing.

FT SIGNAL 1 19

FT CHAIN 20 93

FT DISULFID 30 55

FT DISULFID 32 71

FT VARSPLIC 90 93

SEQUENCE 93 AA: 10581 MW: 44FC763711B9B37 CR664;

Query Match

Best Local Similarity 97.0%; Score 341; DB 1; Length 93;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 KGVSLSPRCPCRFESHVARANKHLKILNTPNCALQIYARLKNNNROYCIDPKLKWIOE 60
DB 22 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIYARLKNNNROYCIDPKLKWIOE 81
QY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 2
SDFL_HUMAN STANDARD: PRT: 93 AA.
AC P48061;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DR 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell
GN growth stimulating factor) (PBSF) (H1RH).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RA Spotila L.D.;
RL Submitted (OCU-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=96039262; PubMed=7490086;
RA Shirozu M., Nakano T., Inazawa J., Tashiro K., Tada H.,
RA Shinohara T., Honjo T.;
RT "Structure and chromosomal localization of the human stromal cell-
RT derived factor 1 (SDF1) gene.";
RL Genomics 28:495-500(1995).
RN [3]
RX SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Liver;
RA Begum N.A., Barnard G.F.;
RT "Nucleotide sequence of h1RH, human interleukin reduced in
RL heptomas.", to the EMBL/GenBank/DBJ databases.
RN [4]
RX STRUCTURE BY NMR OF 22-88.
RA MEDLINE=98046030; PubMed=9384579;
RA Crump M.P., Gong J.H., Loetscher P., Rajaratnam K., Amara A.,
RA Arenzana-Seisdedos F., Virelizier J.L., Baggiolini M., Stiles B.D.,
RA Clark-Lewis I.;
RT "Solution structure and basis for functional activity of stromal
RT cell-derived factor-1; dissociation of CXCR4 activation from binding
RT and inhibition of HIV-1.";
RL EMBO J. 16:6996-7007(1997).
RN [5]
RX X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-88.
RA MEDLINE=98284037; PubMed=9618518;
RA Dealwis C., Fernandez E.J., Thompson D.A., Simon R.J., Slani M.A.,
RA Lolis E.;
RT "Crystal structure of chemically synthesized [N33A] stromal
RT cell-derived factor 1alpha, a potent ligand for the HIV-1 'fusin'
RT coreceptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:6941-6946(1998).
RN [6]
RX FUNCTION: CHEMOTACTICANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT
RN NOT NEUTROPHILS.
RN [7]
RX ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE);
RN -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
RN C-X-C) (CHEMOKINE CXC).
RN [8]
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DB -----
DR EMBL: U16752; AAA97434.1; -
DR EMBL: U16752; AAA97434.1; -
DR EMBL: U16752; AAA97434.1; -
DR EMBL: U16752; AAA97434.1; -
DR EMBL: U16752; AAA97434.1; -
DR EMBL: U16752; AAA97434.1; -
DR PDB: 1SDE; 28-JAN-98.
DR PDB: 2SDE; 17-JUN-98.
DR PDB: 1A15; 12-AUG-98.
DR Genew: HGNC:10672; SDF1.
DR MIM: 600835;
DR InterPro: IPR001089; CXC_c1mkline.sm11.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
KW Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing;
KW 3D-structure.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 93 STROMAL CELL-DERIVED FACTOR 1.
FT DISULFID 30 55
FT DISULFID 32 71
FT VARSPIC 90 93 MISSING (IN ISOFORM ALPHA).
SQ SEQUENCE 93 AA; 10666 MW; 505B5A29C2B44E8D CRC64;

Query Match 95.0%; Score 341; DB 1; Length 93;
Best Local Similarity 97.0%; Pred. No. 6; le-35;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSPRCPCRFESHVARANKHLKILNTPNCALQIYARLKNNNROYCIDPKLKWIOE 60
DB 22 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIYARLKNNNROYCIDPKLKWIOE 81
QY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 3
SDFL_MOUSE STANDARD: PRT: 89 AA.
AC P40224;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DR 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell
DE growth stimulating factor) (PBSF) (12-O-tetradecanoylphorbol 13-
DE acetate repressed protein 1) (TPAR1) (Thymic lymphoma cell stimulating
DE factor) (TISF).
GN SDF1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX SEQUENCE FROM N.A.
RA MEDLINE=94181581; PubMed=8134392;
RA Nagasawa T., Kikutani H., Kishimoto T.;
RT "Molecular cloning and structure of a pre-B-cell growth-stimulating
RT factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:2305-2309(1994).
RN [2]
RX SEQUENCE FROM N.A.
RA MEDLINE=93342488; PubMed=8342023;
RA Tashiro K., Tada H., Heller R., Shirozu M., Nakano T., Honjo T.;
RT "Signal sequence trap: a cloning strategy for secreted proteins and
RT type I membrane proteins.";
RL Science 261:600-603(1993).
RN [3]
RX SEQUENCE FROM N.A.
RA MEDLINE=95073497; PubMed=7982471;
RA Jiang W., Zhou P., Kahn S.M., Tomita N., Johnson M.D.,

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RA Wellstein I.B.:  
 RT "Molecular cloning of TPARI, a gene whose expression is repressed by  
 the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA).";  
 RL Exp. Cell Res. 215:284-293(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-AKR/J;  
 RA Nomura M., Nakata Y., Uzuwa A., Nose M., Akashi M., Suzuki G.:  
 RL Submitted (DEC-1994) to the EMBL/Genbank/DBD databases.  
 CC -1- FUNCTION: CHEMOATTRACTANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT  
 NOT NEUTROPHILS.  
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF BONE MARROW-DERIVED B  
 PROGENITOR CELLS IN THE PRESENCE OF IL-7 AS WELL AS GROWTH OF THE  
 CC STROMAL CELL-DEPENDENT B-CELL CLONE DM34 CELLS.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE);  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: BELONGS TO THE INTERKINE ALPHA FAMILY (SMALL CYTOKINE  
 C-X-C) (CHEMOKINE CXCL).  
 CC -----  
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 CC -----  
 DR EMBL: D21072; BAA04648.1; -  
 DR EMBL: L12029; AAA40100.1; -  
 DR EMBL: L12030; AAA40101.1; -  
 DR EMBL: S74318; AAB32650.1; -  
 DR EMBL: D43804; BAA07862.1; -  
 DR EMBL: D43805; BAA07863.1; -  
 DR PIR: A53497; A53497.  
 DR HSSP: P48061; ISDF.  
 DR MGD: MGI:103556; Sdfl.  
 DR InterPro: IPR001089; CXCL\_cmnkine\_sm1.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PF00048; IL8; 1.  
 DR SMART: SM00199; SCY; 1.  
 DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; FALSE\_NEG.  
 DR Cytokine: Chemotaxis; Growth factor; Signal; Alternative splicing.  
 FT SIGNAL 1 19  
 FT CHAIN 20 89 STROMAL CELL-DERIVED FACTOR 1.  
 FT DISULFID 30 55  
 FT DISULFID 32 71 BY SIMILARITY.  
 FT VARSPLIC 89 89 K -> KRLKM (IN ISOFORM BETA).  
 SQ SEQUENCE 89 AA: 10032 MW: C48BAD69078E55FA CRC64;  
 Query Match 94.7%; Score 340; DB 1; Length 89;  
 Best Local Similarity 95.5%; Pred. No. 7.7e-35;  
 Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 KGVSLSPRCPCRFESHVARANKHLINTPNCALQIVARLKNNRQVCIDPKLWIOE 60  
 DB 22 KPVSLSPRCPCRFESHVARANKHLINTPNCALQIVARLKNNRQVCIDPKLWIOE 81  
 QY 61 YLEKALN 67  
 DB 82 YLEKALN 88  
 RESULT 4  
 IL8\_CANVO STANDARD: PRT; 101 AA.  
 AC P49113;  
 DT 01-FEB-1996 (rel. 33, Created)  
 DT 01-FEB-1996 (rel. 33, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE Interleukin-8 precursor (IL-8) (CXCL8) (Neutrophil attractant protein  
 DE 1) (NAP-1).  
 GN IL8.  
 OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.  
 OC NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Spleen;  
 RA MEDLINE-94065176; PubMed-7504015;  
 RX Yoshimura T., Johnson D.G.:  
 RT "CDNA cloning and expression of guinea pig neutrophil attractant  
 RT protein-1 (NAP-1). NAP-1 is highly conserved in guinea pig.";  
 RL J. Immunol. 151:6225-6236(1993).  
 CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,  
 CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN  
 CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN  
 CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE INTERKINE ALPHA FAMILY (SMALL CYTOKINE  
 CC C-X-C) (CHEMOKINE CXCL).  
 CC -----  
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 CC -----  
 DR EMBL: L04986; AAA37049.1; -  
 DR HSSP: P10145; 2IL8.  
 DR InterPro: IPR001089; CXCL\_cmnkine\_sm1.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTKCXC.  
 DR SMART: SM00199; SCY; 1.  
 DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; 1.  
 DR Cytokine: Chemotaxis; Inflammatory response; signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 101 INTERLEUKIN-8.  
 FT DISULFID 34 61 BY SIMILARITY.  
 FT DISULFID 36 77 BY SIMILARITY.  
 SQ SEQUENCE 101 AA: 11414 MW: 557E2A9E15F6727F CRC64;  
 Query Match 28.1%; Score 101; DB 1; Length 101;  
 Best Local Similarity 35.9%; Pred. No. 1.4e-05;  
 Matches 23; Conservative 16; Mismatches 17; Indels 8; Gaps 5;  
 QY 8 RCPGRFESHVARAN--VKHLKILNT-PNCA-LQIVARLKNNRQVCIDPKLWIOEYL 62  
 DB 33 RCQC--IKIHTPFHKPIKELKLVIESGPCANSEILVKL-SNROLCIDPKKKWQDVY 89  
 QY 63 EKAL 66  
 DB 90 SMFL 93  
 RESULT 5  
 IL8\_CANFA STANDARD: PRT; 101 AA.  
 AC P41324;  
 DT 01-FEB-1995 (rel. 31, Created)  
 DT 01-FEB-1995 (rel. 31, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE Interleukin-8 precursor (IL-8) (CXCL8).  
 GN IL8.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OC NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-94010328; PubMed-7916715;  
 RX Ishikawa J., Suzuki S., Hotta K., Hirota Y., Mizuno S., Suzuki K.:  
 RT "Cloning of a canine gene homologous to the human

RT interleukin-8-encoding gene.";  
 RL Gene 131:305-306(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-lymph node;  
 RX MEDLINE=95127913; PubMed=7827282;  
 RA Matsumoto Y., Mohamed A., Onodera T., Kato H., Ohashi T.,  
 RA Goitaka R., Tsujimoto H., Hasegawa A., Furusawa S., Yoshinara K.,  
 RA Ishikawa J., Hotta K., Suzuki K., Hirota Y.;  
 RT "Molecular cloning and expression of canine interleukin 8 cDNA.";  
 RL Cytokine 6:455-461(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Mongrel; TISSUE=Jugular vein;  
 RX MEDLINE=95114148; PubMed=7814650;  
 RA Kukialka G.L., Smith W.C., Larosa G.J., Manning A.M.,  
 RA Mendoza L.H., Daly T.J., Hughes B.J., Youker K.A., Hawkins H.K.,  
 RA Michael L.H., Rot A., Entman M.L.;  
 RT "Interleukin-8 gene induction in the myocardium after ischemia and  
 RT reperfusion in vivo.";  
 RL J. Clin. Invest. 95:89-103(1995).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Beagle;  
 RX MEDLINE=97230298; PubMed=9119462;  
 RA Straubinger R.R., Straubinger A.F., Harter L., Jacobson R.H.,  
 RA Chang Y.-F., Summers B.A., Erb H.N., Appel M.J.;  
 RT "Borrelia burgdorferi migrates into joint capsules and causes an up-  
 RT regulation of interleukin-8 in synovial membranes of dogs  
 RT experimentally infected with ticks.";  
 RL Infect. Immun. 65:1273-1285(1997).  
 CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,  
 CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN  
 CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN  
 CC RESPONSE TO AN INFLAMMATORY STIMULUS.  
 CC -1- SUBUNIT: HOMODIMER. (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE  
 CC C-X-C) (CHEMOKINE CX-C).  
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 CC -----  
 DR EMBL: D28772; BAA05961.1; -;  
 DR EMBL: D14285; BAA03246.1; -;  
 DR EMBL: U10308; AAC48434.1; -;  
 DR EMBL: AF048717; AAC05134.1; -;  
 DR HSSP: P10145; 1IKM.  
 DR InterPro: IPR001089; CXC\_Chemkine\_sm1.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTRKXC.  
 DR SMART: SM00199; SCY; 1.  
 DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; 1.  
 KW CYTOKINE; Chemotaxis; Inflammatory response; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 101 BY SIMILARITY.  
 FT DISULFID 34 61 INTERLEUKIN-8.  
 FT DISULFID 36 77 BY SIMILARITY.  
 SQ SEQUENCE 101 AA; 11280 MW; 3A3A4676DA968376 CRC64;  
 Query Match 27.6%; Score 99; DB 1; Length 101;  
 Best Local Similarity 36.1%; Pred. No. 2.5e-05;  
 Matches 26; Conservative 15; Mismatches 19; Indels 12; Gaps 5;  
 OY 3 VSISPRPCPFESHVARVKNHLKILNT-----PNCALQIVARLKNKNROVCIIDPLKRW 57  
 DB 28 VSSELKRCQ--IKTHSPFPKPIKELRVIDSQPHCENSEIIVKLVNGN-EVCLDPKRW 84

OY 58 IQE----YLEKA 65  
 DB 85 VQKVQVIFLAKKA 96  
 RESULT 6  
 ID IL8\_FELCA STANDARD; PRT; 101 AA.  
 AC O9XSX5;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE Interleukin-8 precursor (IL-8) (CXCL8).  
 GN IL8.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_Taxid=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Straubinger A.F., Simpson K.W., Straubinger R.K.;  
 RT "Feline interleukin-8 mRNA.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,  
 CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN  
 CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN  
 CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE  
 CC C-X-C) (CHEMOKINE CX-C).  
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 CC -----  
 DR EMBL: AF158598; AAD40323.1; -;  
 DR HSSP: P10145; 1IKM.  
 DR InterPro: IPR001089; CXC\_Chemkine\_sm1.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTRKXC.  
 DR SMART: SM00199; SCY; 1.  
 DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; 1.  
 KW CYTOKINE; Chemotaxis; Inflammatory response; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 101 BY SIMILARITY.  
 FT DISULFID 34 61 INTERLEUKIN-8.  
 FT DISULFID 36 77 BY SIMILARITY.  
 SQ SEQUENCE 101 AA; 11165 MW; 690D97F13EF79170 CRC64;  
 Query Match 26.7%; Score 96; DB 1; Length 101;  
 Best Local Similarity 33.3%; Pred. No. 5.8e-05;  
 Matches 22; Conservative 18; Mismatches 18; Indels 8; Gaps 5;  
 OY 3 VSISPRPCPFESHVARAN---VKHLKILNT-PNCALQIVARLKNKNROVCIIDPLKRW 57  
 DB 28 VSSELKRCQ--IKTHSPFPKPIKELRVIDSQPHCENSEIIVKLV-NGKEVCIDPKRW 84  
 OY 58 IOEYLE 63  
 DB 85 VQKVVE 90  
 RESULT 7  
 ID IL8\_HUMAN STANDARD; PRT; 99 AA.  
 AC P10145; O9C077; O96RG6;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE Interleukin-8 precursor (IL-8) (CXCL8) (Monocyte-derived neutrophil-  
 DE chemotactic factor) (MDCNF) (T-cell chemotactic factor) (Neutrophil-  
 DE activating protein 1) (NAP-1) (Lymphocyte-derived neutrophil-  
 DE activating factor) (LYNAP) (Protein 3-10C) (Neutrophil-activating  
 DE factor) (NAF) (Granulocyte chemotactic protein 1) (GCP-1) (Emotactin).  
 GN IL8.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid:9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-88258376; PubMed-3260265;  
 RA Matsushima K., Morishita K., Yoshimura T., Iavv S., Kobayashi Y.,  
 RA Lew W., Appella E., Kung H., Leonard E.J., Oppenheim J.J.;  
 RT "Molecular cloning of a human monocyte-derived neutrophil chemotactic  
 RT factor (MDCNF) and the induction of MDCNF mRNA by interleukin 1 and  
 RT tumor necrosis factor.";  
 RL J. Exp. Med. 167:1883-1893(1988).  
 RN (12)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-87224164; PubMed-2953813;  
 RA Schmidt J., Weismann C.;  
 RT "Induction of mRNA for a serine protease and a  
 RT beta-thromboglobulin-like protein in mitogen-stimulated human  
 RT leukocytes.";  
 RL J. Immunol. 139:250-256(1987).  
 RN (13)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-89313739; PubMed-2664463;  
 RA Kowalski J., Denhardt D.T.;  
 RT "Regulation of the mRNA for monocyte-derived neutrophil-activating  
 RT peptide in differentiating HL60 promyelocytes.";  
 RL Mol. Cell. Biol. 9:1946-1957(1989).  
 RN (14)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-89309826; PubMed-2663993;  
 RA Mukai N., Shiro M., Matsushima K.;  
 RT "Genomic structure of the human monocyte-derived neutrophil  
 RT chemotactic factor IL-8.";  
 RL J. Immunol. 143:1366-1371(1989).  
 RN (15)  
 RP SEQUENCE FROM N.A.  
 RA Ishikawa J.;  
 RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.  
 RN (16)  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RA Jang J.S., Kim B.E.;  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 RN (17)  
 RP SEQUENCE FROM N.A.  
 RA Rieder M.J., Carlington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi O.,  
 RA Nickerson D.A.;  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RN (18)  
 RP SEQUENCE OF 23-46.  
 RX MEDLINE-89246368; PubMed-2655563;  
 RA Goids E.E., Mason P., Nyirkos P.;  
 RT "Inflammatory cytokines induce synthesis and secretion of gro protein  
 RT and a neutrophil chemotactic factor but not beta 2-microglobulin in  
 RT human synovial cells and fibroblasts.";  
 RL Biochem. J. 259:585-588(1989).  
 RN (19)  
 RP SEQUENCE OF 23-54.  
 RX MEDLINE-89279141; PubMed-2659722;  
 RA Suzuki K., Miyasaka H., Ota H., Yamakawa Y., Tagawa M., Kuramoto A.,  
 RA Mizuno S.;  
 RT "Purification and partial primary sequence of a chemotactic protein  
 RT for polymorphonuclear leukocytes derived from human lung giant cell  
 RT carcinoma L065C cells.";  
 RL J. Exp. Med. 169:1895-1901(1989).  
 RN (10)

RP SEQUENCE OF 28-99.  
 RX MEDLINE-88162914; PubMed-3279957;  
 RA Gregory H., Young J., Schroeder J.M., Mrowietz U., Christophers E.;  
 RT "Structure determination of a human lymphocyte derived neutrophil  
 RT activating peptide (LYNAP).";  
 RL Biochem. Biophys. Res. Commun. 151:883-890(1988).  
 RN (11)  
 RP SEQUENCE OF 28-59.  
 RX MEDLINE-88106502; PubMed-3322281;  
 RA Walz A., Pevert P., Aschauer H., Baggiolini M.;  
 RT "Purification and amino acid sequencing of NAF, a novel neutrophil-  
 RT activating factor produced by monocytes.";  
 RL Biochem. Biophys. Res. Commun. 149:755-761(1987).  
 RN (12)  
 RP SEQUENCE OF 28-69.  
 RX MEDLINE-88097462; PubMed-3480540;  
 RA Yoshimura T., Matsushima K., Tanaka S., Robinson E.A., Appella E.,  
 RA Oppenheim J.J., Leonard E.J.;  
 RT "Purification of a human monocyte-derived neutrophil chemotactic  
 RT factor that has peptide sequence similarity to other host defense  
 RT cytokines.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:9233-9237(1987).  
 RN (13)  
 RP N-TERMINAL FORMS.  
 RX MEDLINE-91006326; PubMed-2145175;  
 RA van Damme J., Rampart M., Coning R., Decock B., van Osselaer N.,  
 RA Willems J., Billiau A.;  
 RT "The neutrophil-activating proteins interleukin 8 and beta-  
 RT thromboglobulin: in vitro and in vivo comparison of NH2-terminally  
 RT processed forms.";  
 RL Eur. J. Immunol. 20:2113-2118(1990).  
 RN (14)  
 RP N-TERMINAL FORMS.  
 RX MEDLINE-89231715; PubMed-2523801;  
 RA van Damme J., van Beeumen J., Conings R., Decock B., Billiau A.;  
 RT "Purification of granulocyte chemotactic peptide/interleukin-8  
 RT reveals N-terminal sequence heterogeneity similar to that of  
 RT beta-thromboglobulin.";  
 RL Eur. J. Biochem. 181:337-344(1989).  
 RN (15)  
 RP SYNTHESIS OF 28-99.  
 RX MEDLINE-91175767; PubMed-2007144;  
 RA Clark-Lewis I., Mose B., Walz A., Baggiolini M., Scott G.J.,  
 RA Aebersold R.;  
 RT "Chemical synthesis, purification, and characterization of two  
 RT inflammatory proteins, neutrophil activating peptide 1  
 RT (interleukin-8) and neutrophil activating peptide.";  
 RL Biochemistry 30:3128-3135(1991).  
 RN (16)  
 RP REVIEW.  
 RX MEDLINE-92347562; PubMed-1639201;  
 RA Baggiolini M., Clark-Lewis I.;  
 RT "Interleukin-8, a chemotactic and inflammatory cytokine.";  
 RL FEBS Lett. 307:97-101(1992).  
 RN (17)  
 RP STRUCTURE BY NMR.  
 RX MEDLINE-90234679; PubMed-2184886;  
 RA Clore G.M., Appella E., Yamada M., Matsushima K., Gronenborn A.M.;  
 RT "Three-dimensional structure of interleukin 8 in solution.";  
 RL Biochemistry 29:1689-1696(1990).  
 RN (18)  
 RP STRUCTURE BY NMR OF COMPLEX TO RECEPTOR.  
 RX MEDLINE-99148123; PubMed-10368283;  
 RA Skelton N.J., Quan C., Reilly D., Lowman H.;  
 RT "Structure of a CXC chemokine-receptor fragment in complex with  
 RT interleukin-8.";  
 RL Structure 7:157-168(1999).  
 RN (19)  
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 RX MEDLINE-90216714; PubMed-2182630;  
 RA Baldwin E.T., Franklin K.A., Appella E., Yamada M., Matsushima K.,  
 RA Wlodawer A., Weber I.T.;  
 RT "Crystallization of human interleukin-8. A protein chemotactic for

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RT neutrophils and T-lymphocytes."
RL J. Biol. Chem. 265:6851-6853(1990).
RN [20]
RP X-RAY CRYSTALLOGRAPHY, AND STRUCTURE BY NMR.
RX MEDLINE-91171286; PubMed-2005614;
RA Clore G.M., Gronenborn A.M.;
RT "Comparison of the solution nuclear magnetic resonance and crystal
RT structures of interleukin-8. Possible implications for the mechanism
RT of receptor binding."
RL J. Mol. Biol. 217:611-620(1991).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS), AND STRUCTURE BY NMR.
RX MEDLINE-91110556; PubMed-1988949;
RA Baldwin E.T., Weber I.T., St Charles R., Xuan J.C., Appella E.,
RA Yamada M., Matsushima K., Edwards B.F., Clore G.M., Gronenborn A.M.;
RT "Crystal structure of interleukin 8: symbiosis of NMR and
RT crystallography."
RL Proc. Natl. Acad. Sci. U.S.A. 88:502-506(1991).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF MUTANT.
RX MEDLINE-20178334; PubMed-10707023;
RA Geiger N., Lowman H., Artis D.R., Eigenbrot C.;
RT "Receptor-binding conformation of the 'ELR' motif of IL-8: X-ray
RT structure of the L5C/H33C variant at 2.35 A resolution."
RL Proteins 38:361-367(2000).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CX-C).
-----
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-----
DR EMBL: Y00787; CA668742.1; -
DR EMBL: M17017; AAA55611.1; -
DR EMBL: M26383; AAA36323.1; -
DR EMBL: M28130; AAA59158.1; -
DR EMBL: D14283; BAA03245.1; -
DR EMBL: AF043337; AAK00048.1; -
DR EMBL: AF385628; AAK60276.1; ALT_SEQ.
DR PIR: A37034; A37034.
DR PIR: S03975; S03975.

Query Match 26.2%; Score 94; DB 1; Length 99;
Best Local Similarity 32.3%; Pred. No. 9.9e-05;
Matches 20; Conservative 18; Mismatches 20; Indels 4; Gaps 4;

OY 8 RCPC-REFESHVAVANVKKILINT-PNCA-LQIVARLNKNNQVCIDPKLKWIOEY 64
DB 33 RCQCIKTSKPRPKIKRLVIESGPHCANTEIIVKL-SDGRELCLDKENNVQVVER 91
OY 65 AL 66
DB 92 FL 93

RESULT 8
ST02_CAVPO STANDARD: PRT; 120 AA.
AC Q08782;
DT 01-NOV-1995 (Rel. 32; Created)
DT 01-NOV-1995 (Rel. 32; Last sequence update)
DT 15-JUL-1999 (Rel. 38; Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1).

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GN SCVA2 OR KCPI.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Z; TISSUE=Spleen;
RX MEDLINE-93267104; PubMed-8496603;
RA Yoshimura T.;
RT "cDNA cloning of guinea pig monocyte chemoattractant protein-1 and
RT expression of the recombinant protein."
RL J. Immunol. 150:5025-5032(1993).
CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES, BUT NOT
CC NEUTROPHILS.
CC -1- SUBUNIT: MONOMER OR HOMODIMER; IN EQUILIBRIUM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
-----
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-----
DR EMBL: I04985; AAA37047.1; -
DR HSP; P80098; IBOO.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
DR Cytokine; Chemotaxis; Signal; Inflammatory response; Glycoprotein.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 120 SMALL INDUCIBLE CYTOKINE A2.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY)
FT DISULFID 33 57 BY SIMILARITY.
FT DISULFID 34 73 BY SIMILARITY.
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 120 AA; 13741 MW; 5905596851CFC154 CRC64;

Query Match 26.2%; Score 94; DB 1; Length 120;
Best Local Similarity 31.7%; Pred. No. 0.00012;
Matches 20; Conservative 12; Mismatches 29; Indels 2; Gaps 2;

OY 2 GVSLSRPCRFESHVAVANVKKILINTPNCA-LQIVARLNKNNRQVCIDPKLKWIOEY 61
DB 27 GVN-PTTC-CYFNKQIDPLKRYKGYERTISSRCQDAVLFRLKNKEVCADFTQKVVQY 84
OY 62 LEK 64
DB 85 IAK 87

RESULT 9
ST05_MOUSE STANDARD: PRT; 91 AA.
AC P30882;
DT 01-JUL-1993 (Rel. 26; Created)
DT 01-JUN-1994 (Rel. 29; Last sequence update)
DT 13-JUN-2002 (Rel. 41; Last annotation update)
DE Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES
DE protein) (SIS-delta) (Murantes).
GN SCVA5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.  
 RX MEDLINE-92277990; PubMed=1375672;  
 RA Heeger P., Wolf G., Meyers C., Sun M.J., O'Farrell S.C.,  
 RA Krensky A.M., Neilson E.G.;  
 RT "Isolation and characterization of cDNA from renal tubular epithelium  
 RT encoding murine Rantes";  
 RN Kidney Int. 41:220-225(1992).  
 RL  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-92289605; PubMed=1376260;  
 RA Schall T.J., Simpson N.J., Mak J.Y.;  
 RT "Molecular cloning and expression of the murine RANTES cytokine;  
 RT structural and functional conservation between mouse and man.";  
 RL Eur. J. Immunol. 22:1477-1481(1992).  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-94132613; PubMed=7507961;  
 RA Danoff T.M., Lalley P.A., Chang Y.S., Heeger P.S., Neilson E.G.;  
 RT "Cloning, genomic organization, and chromosomal localization of the  
 RT Scv55 gene encoding the murine chemokine RANTES";  
 RL J. Immunol. 152:1182-1189(1994).  
 RN  
 RP SEQUENCE FROM N.A.  
 RX STRAIN-BALB/c;  
 RC MEDLINE-94217689; PubMed=7513046;  
 RA Shih H.S., Drysdale B.E., Shih M.L., Noble P.W., Fisher S.N.,  
 RA Paznekas W.A.;  
 RT "Definition of a lipopolysaccharide-responsive element in the 5'-  
 RT flanking regions of Muranes and crg-2";  
 RL Mol. Cell. Biol. 14:2914-2925(1994).  
 RN  
 RP SEQUENCE FROM N.A.  
 RX STRAIN-BALB/c; BIO.S/J, NOB/LTJ, and SJL/J; TISSUE=Spleen;  
 RA Ma R.Z., Teuscher C.;  
 RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.  
 CC -I- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER  
 CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM  
 CC BASOPHILS AND ACTIVATES EOSINOPHILS.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- TISSUE SPECIFICITY: T-CELL AND MACROPHAGE SPECIFIC.  
 CC -I- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE  
 CC C-C) (CHEMOKINE CC).  
 CC -----  
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 CC -----  
 CC  
 DR EMBL: M77747; AAA40029.1; -;  
 DR EMBL: S37648; AAB22330.1; -;  
 DR EMBL: U02298; AAA18302.1; -;  
 DR EMBL: X70675; CAA50011.1; -;  
 DR EMBL: AF065944; AAC17511.1; -;  
 DR EMBL: AF065945; AAC17512.1; -;  
 DR EMBL: AF065946; AAC17513.1; -;  
 DR EMBL: AF065947; AAC17514.1; -;  
 DR HSSP: P13501; IRTN.  
 DR MGD: MGI:98262; Scv55.  
 DR Interpro: IPR000827; CC.Chemokine.sml.  
 DR Interpro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PF00048; IL8; 1.  
 DR SMART: SM00199; SCV; 1.  
 DR PROSITE: PS00472; SMALL\_CYTOKINES\_CC; 1.  
 KW Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.  
 FT SIGNAL 1 23  
 FT CHAIN 24 91  
 FT DISULFID 33 57  
 FT DISULFID 34 73  
 FT CONFLICT 19 19 T -> A (IN REF. 2).

FT CONFLICT 41 41 A -> E (IN REF. 1).  
 SQ SEQUENCE. 91 AA: 10071 MW: 5DFD66F44684FEEC8 CRC64;  
 Query Match 25.5%; Score 91.5; DB 1; Length 91;  
 Best Local Similarity 37.3%; Pred. NO. 0.0018;  
 Matches 22; Conservative 9; Mismatches 25; Indels 3; Gaps 2;  
 QY 6 SPRCPREFESHA--RAVVKHLKILTPNCALQIYARLKNRRVOCIDPKLWIOEYL 62  
 DB 28 SPTTCCFAVYLSLALPRAHVKY-FYTSSKCSNLAVVFYTRRRVOCANPEKKWQYEYI 85  
 RESULT 10  
 ID SY05\_RAT STANDARD; PRT; 92 AA.  
 AC P50231;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES  
 DE protein) (SIS-delta).  
 OS SCV55.  
 GN Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=Long Evans; TISSUE=Lung;  
 RA Jones M.L., Shanley T.P., Ward P.A.;  
 RL Submitted (FEB-1994) to the EMBL/Genbank/DBJ databases.  
 CC -I- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER  
 CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM  
 CC BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE  
 CC C-C) (CHEMOKINE CC).  
 CC -----  
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 CC -----  
 CC  
 DR EMBL: U06436; AAA96499.1; -;  
 DR HSSP: P13501; IRTN.  
 DR Interpro: IPR000827; CC.Chemokine.sml.  
 DR Interpro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PF00048; IL8; 1.  
 DR SMART: SM00199; SCV; 1.  
 DR PROSITE: PS00472; SMALL\_CYTOKINES\_CC; 1.  
 KW Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.  
 FT SIGNAL 1 24  
 FT CHAIN 25 92  
 FT DISULFID 34 58  
 FT DISULFID 35 74  
 FT DISULFID 74 74 BY SIMILARITY.  
 SQ SEQUENCE 92 AA: 10170 MW: B4FEC2B4208ABC6 CRC64;  
 Query Match 25.5%; Score 91.5; DB 1; Length 92;  
 Best Local Similarity 37.3%; Pred. NO. 0.00019;  
 Matches 22; Conservative 9; Mismatches 25; Indels 3; Gaps 2;  
 QY 6 SPRCPREFESHA--RAVVKHLKILTPNCALQIYARLKNRRVOCIDPKLWIOEYL 62  
 DB 29 SPTTCCFAVYLSLALPRAHVKY-FYTSSKCSNLAVVFYTRRRVOCANPEKKWQYEYI 86  
 RESULT 11  
 GRO\_MOUSE STANDARD; PRT; 96 AA.  
 AC P12850;

DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Growth regulated protein precursor (CXCL1) (Platelet-derived growth factor-induced protein KC) (Secretory protein N51).  
 GN SCYB1 OR GRO1 OR GRO OR MGA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89139485; PubMed=2917992;  
 RA Oquendo P., Alberta J., Wen D., Graycar J.L., Derynck R., Stiles C.D.;  
 RT "The platelet-derived growth factor-inducible KC gene encodes a secretory protein related to platelet alpha-granule proteins.";  
 RL J. Biol. Chem. 264:4133-4137(1989).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89078502; PubMed=290392;  
 RA Ryseck R.P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;  
 RT "Cloning and sequence of a secretory protein induced by growth factors in mouse fibroblasts";  
 RL Exp. Cell Res. 180:266-275(1989).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/Sv;  
 RA Bozic C.R., Kolakowski L.F., Jr., von Duxkull C., Garcia-Rodriguez M., Conklyn M.J., Breslow R., Showell H.J., Gerard N.P., Gerard C.;  
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.  
 RN (4)  
 RP SEQUENCE OF 1-10 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=96016008; PubMed=7561058;  
 RA Omori Y., Fukumoto S., Hamilton T.A.;  
 RT "Two structurally distinct kappa B sequence motifs cooperatively control LPS-induced KC gene transcription in mouse macrophages";  
 RL J. Immunol. 155:3593-3600(1995).  
 CC -1- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. CONTRIBUTES TO NEUTROPHIL ACTIVATION DURING INFLAMMATION (BY SIMILARITY).  
 CC -1- INDUCTION: BY PLATELET-DERIVED GROWTH FACTOR. IN LUNG, BY LIPOPOLYSACCHARIDE OR INFLAMMATION (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXK).  
 CC -----  
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 CC -----  
 DR EMBL: J04596; AAA0131.1; -;  
 DR EMBL: U20634; AAB0376.1; -;  
 DR EMBL: U20527; AAB0376.1; JOINED.  
 DR EMBL: S79767; -; NOT\_ANNOTATED\_CDS.  
 DR PIR: A32954; A32954.  
 DR PIR: JH0081; JH0081.  
 DR HSSP: P19875; IQNK.  
 DR MGD: MGI:108068; Gro1.  
 DR InterPro: IPR001089; CXK\_cmkline\_sm1.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTKCXK.  
 DR SMART: SM00199; SCY; 1.  
 DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; 1.  
 KW Cytokine; Growth factor; Inflammatory response; Signal.  
 FT CHAIN 1 24 PROBABLE.  
 FT DISULFID 33 59 BY SIMILARITY.  
 FT DISULFID 33 59 BY SIMILARITY.  
 SQ SEQUENCE 96 AA; 10254 MW; 4A52B5E5C38B45C2 CRC64;

Query Match 25.5%; Score 91.5; DB 1; Length 96;  
 Best Local Similarity 32.8%; Pred. No. 0.00019;  
 Matches 20; Conservative 17; Mismatches 21; Indels 3; Gaps 3;  
 Oy 8 RCPGRFFSHVARNANKHLKIL-NTPNCA-LQIVARKNNRQYCIDPKKIQIETLEKA 65  
 Db 32 RCOCLQTMAGIHKNIOSLKVLPSGPHCTQTEVIATLK-NGRACIDPEAPLVQKIVQM 90  
 Oy 66 L 66  
 Db 91 L 91  
 RESULT 12  
 IL8\_MACMU STANDARD; PRT; 101 AA.  
 AC P51495;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-8 precursor (IL-8) (CXCL8).  
 GN IL8.  
 OS Macaca mulatta (Rhesus macaque), and  
 OC Macaca nemestrina (Pig-tailed macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9544, 9545.  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=96003435; PubMed=7561102;  
 RA Vallinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;  
 RT "Comparative sequence analysis of cytokine genes from human and nonhuman primates";  
 RL J. Immunol. 155:3946-3954(1995).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M.mulatta; TISSUE=Blood;  
 RX MEDLINE=95353132; PubMed=7628861;  
 RA Minnerly J.C., Bagantof M.P., Deppeler C.L., Keller B.T., Rapp S.R., Wlowski D.L., Frelund D.J., Bolanowski M.A.;  
 RT "Identification and characterization of rhesus macaque interleukin-8";  
 RL Interleukin 19:313-331(1995).  
 CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS, BASOPHILS, AND T-CELLS. IT IS ALSO INVOLVED IN NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXK).  
 CC -----  
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 CC -----  
 DR EMBL: U19849; AAA6711.1; -;  
 DR EMBL: U19851; AAA6713.1; -;  
 DR EMBL: S78555; AAA80141.2; -;  
 DR HSSP: P10145; 2IL8.  
 DR InterPro: IPR001089; CXK\_cmkline\_sm1.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTKCXK.  
 DR SMART: SM00199; SCY; 1.  
 DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; 1.  
 KW Cytokine; Chemotaxis; Inflammatory response; Signal.

FT	DISUFLID	36	77	BY SIMILARITY
SC	SEQUENCE	101 AA:	11292 MM:	40E8418B57C56A5B CRC64:
	Query Match		25.3%:	Score 91: DB 1: Length 101:
	Best Local Similarity		30.4%:	Pred. No. 0.00024:
	Matches	21: Conservative	20: Mismatches	20: Indels 8: Gaps 5:
QY	3 VLSRRCRCRFFESVAVAN--VKHKILNT-PRCA-LQIVARLKNRRNOYCIDPKLKW	57		
DB	28 MSTEELKCC--IKTHSPFHPKFIKELRVIESGPCENSELIIVKL-TNGKEVCIDPKKEKW	84		
QY	58 IOEYLEKAL	66		
DB	85 VQKVAQAF	93		
	RESULT 14			
IL8_PIG	IL8_PIG	STANDARD:	PRT:	103 AA.
AC	P26894:	P22951:		
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Interleukin-8 precursor (IL-8) (CXCL8) (Alveolar macrophage chemotactic factor I) (AMCP-I).			
GN	IL8.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.			
OX	NCBI_TaxID:9823;			
RN	SEQUENCE FROM N.A.			
RX	MDLINE=94103307; Pubmed=8276681;			
RA	Lin G., Pearson A.E., Scamurra R.W., Zhou Y., Baarsch M.J., Weiss D.J., Murtaugh M.P.;			
RT	"Regulation of interleukin-8 expression in porcine alveolar macrophages by bacterial lipopolysaccharide.";			
RL	J. Biol. Chem. 269:77-85(1994).			
RN	SEQUENCE FROM N.A.			
RP	Sanjanwala M.;			
RL	Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.			
RN	SEQUENCE FROM N.A., AND SEQUENCE OF 26-45.			
RC	TISSUE=Lung;			
RX	MDLINE=93041741; Pubmed=1420165;			
RA	Goodman R.B., Foster D.C., Mathewes S.L., Osborn S.G., Kuiper J.L., Forstrom J.W., Martin T.R.;			
RT	"Molecular cloning of porcine alveolar macrophage-derived neutrophil chemotactic factors I and II; identification of porcine IL-8 and another intercrine-alpha protein.";			
RL	Biochemistry 31:10483-10490(1992).			
RN	REVISION TO 23.			
RP	Goodman R.B.;			
RL	Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.			
RN	SEQUENCE OF 26-45.			
RC	STRAIN=Yorkshire;			
RX	MDLINE=91217086; Pubmed=1850745;			
RA	Goodman R.B., Forstrom J.W., Osborn S.G., Chi E.Y., Martin T.R.;			
RT	"Identification of two neutrophil chemotactic peptides produced by porcine alveolar macrophages.";			
RL	J. Biol. Chem. 266:8455-8463(1991).			
CC	-I- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS, BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN RESPONSE TO AN INFLAMMATORY STIMULUS.			
CC	-I- SUBUNIT: HOMODIMER.			
CC	-I- TISSUE SPECIFICITY: ALVEOLAR MACROPHAGES.			
CC	-I- INDUCTION: BY LIPOLYSACCHARIDE (LPS).			
CC	-I- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXCL).			

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CC  
DR EMBL: M86923; AAA16616.1; -  
DR EMBL: X61151; CAA43461.1; -  
DR EMBL: M9367; AAA92576.1; -  
DR PIR: A44253; A44253.  
DR PIR: A39819; A39819.  
DR HSP: P10145; 1IKM.  
DR Interpro: IPR001089; CXC\_chemkine\_sml.  
DR Interpro: IPR001811; Chemokine\_IL8.  
DR Pfam: PF00048; IL8; 1.  
DR SMART: SM00437; SMALLCYTKCXC.  
DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; 1.  
DR Cytokine; Chemotaxis; Inflammatory response; Signal.  
FT SIGNAL 1 25  
FT CHAIN 26 103 INTERLEUKIN-8.  
FT DISULFID 34 61 BY SIMILARITY.  
FT DISULFID 36 77 BY SIMILARITY.  
FT CONFLICT 33 34 RC -> CR (IN REF. 5).  
FT CONFLICT 87 87 K -> KK (IN REF. 2).  
SQ SEQUENCE 103 AA; 11633 MW; 9FEE0350E1928C64 CRC64;  
  
Query Match 25.1%; Score 90; DB 1; Length 103;  
Best Local Similarity 31.8%; Pred. No. 0.00032;  
Matches 21; Conservative 18; Mismatches 19; Indels 8; Gaps 5;  
  
OY 3 VSPPCPCRFEEFESHVARN---VKHLKILNT-PNCA-LQIVARLKNNRQVCIIDPKIKW 57  
DB 28 VSHELKQCQ--INTHSTPHPKFKELRYIESGPHCENSEITVIVL-NKEYVCLDPKRW 84  
OY 58 IOEYLE 63  
DB 85 VQKVVO 90  
  
RESULT 15  
SY05\_CAVPO STANDARD; PRT; 91 AA.  
AC P97272; O09076;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES  
DE protein) (SIS-delta).  
GN SCYA5.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Dunkin-Hartley;  
RA Campbell E.M., Proudfoot A.E.I., Yoshimura T., Allet B.,  
RA Wells T.N.C., White A.M., Westwick J., Watson M.L.;  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Lung;  
RA Asano K., Nakamura M., Oguma T., Fukunaga K., Ishizaka A.,  
RA Yamaguchi K., Kanazawa M.;  
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES. MEMORY T HELPER  
CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM  
CC BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Secreted.

-----  
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE  
CC C-C) (CHEMOKINE CC).  
CC  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC  
DR EMBL: U77037; AAC53293.1; -  
DR EMBL: AB002662; BAA19604.1; -  
DR HSP: P13501; 1RTN.  
DR Interpro: IPR000827; CC\_chemkine\_sml.  
DR Interpro: IPR001811; Chemokine\_IL8.  
DR Pfam: PF00048; IL8; 1.  
DR SMART: SM00199; SCY; 1.  
DR PROSITE: PS00472; SMALL\_CYTOKINES\_CC; 1.  
DR Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.  
FT SIGNAL 1 23  
FT CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5.  
FT DISULFID 33 57 BY SIMILARITY.  
FT DISULFID 34 73 BY SIMILARITY.  
SQ SEQUENCE 91 AA; 10088 MW; 7F6A31B751237DB9 CRC64;  
  
Query Match 24.7%; Score 88.5; DB 1; Length 91;  
Best Local Similarity 33.3%; Pred. No. 0.00043;  
Matches 20; Conservative 14; Mismatches 21; Indels 5; Gaps 3;  
  
OY 6 SPSPCPCRFEEFESHVARNV-HLK--ILNTPNCALQIVARLKNNRQVCIIDPKIKWIOEYL 62  
DB 28 SPTPCCF--AVISRALPRTHIKEYFTSSKSNLAIVFVTRKNRQVCANPEKKWREYI 85  
  
Search completed: January 23, 2003, 15:34:19  
Job time : 6 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 23, 2003, 15:30:38 : Search time 22.6 Seconds  
(without alignments)  
610.848 Million cell updates/sec

Title: US-09-852-424-4  
Perfect score: 359  
Sequence: 1 KGVSLSPRCPCRFESHVAR.....QVCIDPKLKIQVLEKALN 67

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP mhc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*  
15: SP virus:\*  
16: SP bacteriophage:\*  
17: SP archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	341	95.0	92	4	Q9H554
2	333	92.8	89	11	Q9QZD1
3	275	76.6	94	13	Q8UJ99
4	94.5	26.3	91	11	Q91ZL1
5	88	24.5	98	13	Q8QCV8
6	88	24.5	109	13	Q90Y59
7	84.5	23.5	134	12	Q9YVA9
8	84.5	23.5	142	12	Q91B37
9	84	23.4	203	12	Q67634
10	81.5	22.7	97	13	Q8QF55
11	81	22.6	95	12	Q98158
12	81	22.6	104	13	Q73912
13	79.5	22.1	97	11	Q92318
14	79.5	22.1	101	13	Q93442
15	79.5	22.1	108	6	Q28724
16	79	22.0	79	4	Q95689

17	79	22.0	148	11	Q9QYD7	Q9QYD7 mus musculus
18	77.5	21.6	363	13	Q9QZT0	Q9QZT0 brachydanio
19	77.5	21.6	1096	13	Q9QZT1	Q9QZT1 brachydanio
20	77	21.4	97	13	Q98T02	Q98T02 oncorhynch
21	76.5	21.3	100	11	Q91ZK9	Q91ZK9 sigmodon hi
22	76.5	21.3	101	11	Q91ZK9	Q91ZK9 sigmodon hi
23	76	21.2	101	13	Q8UW91	Q8UW91 tritaxus scf
24	76	21.2	106	11	Q92292	Q92292 cricetus
25	73.5	20.5	126	11	Q99J60	Q99J60 mus musculus
26	73.5	20.5	883	13	Q91493	Q91493 torpedo cal
27	73	20.3	102	6	Q95M27	Q95M27 ovis aries
28	72.5	20.2	89	13	Q918E0	Q918E0 gallus gall
29	71.5	19.9	601	13	Q73928	Q73928 scyllorhinu
30	70.5	19.6	91	13	Q8QGS6	Q8QGS6 gallus gall
31	70.5	19.6	97	6	Q9TTS6	Q9TTS6 bos taurus
32	70	19.5	80	4	Q14745	Q14745 homo sapien
33	70	19.5	91	13	Q8QGS7	Q8QGS7 gallus gall
34	70	19.5	92	6	Q8S040	Q8S040 felis silve
35	69.5	19.4	100	6	Q9TTO4	Q9TTO4 equus caball
36	69	19.2	93	4	Q96168	Q96168 homo sapien
37	69	19.2	96	13	Q90825	Q90825 gallus gall
38	69	19.2	395	11	Q91V44	Q91V44 mus musculus
39	67.5	18.8	116	11	Q91ZB2	Q91ZB2 mus musculus
40	67.5	18.8	150	11	Q9QW66	Q9QW66 mus sp. dys
41	67.5	18.8	258	11	Q9D6J7	Q9D6J7 mus musculus
42	67.5	18.8	622	4	Q02295	Q02295 homo sapien
43	67.5	18.8	3685	4	Q14205	Q14205 homo sapien
44	66.5	18.5	101	11	Q9EP62	Q9EP62 ratius norv
45	66	18.4	92	11	Q91Z65	Q91Z65 sigmodon hi

## ALIGNMENTS

RESULT 1  
ID Q9H554 PRELIMINARY: PRT: 92 AA.  
AC Q9H554:  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE BA20J15.1.2 (Stromal cell-derived factor 1, isoform beta)  
DE (Fragment).  
GN SDF1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bird C.;  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL137026; CAC10202.1; -.  
DR HSSP; P48061; ISDP.  
DR InterPro: IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR SMART; SM00199; SCY; 1.  
FT NON\_TER  
SQ SEQUENCE 92 AA; 10510 MW; AEF0C402B44EBD20 CRC64;

Query Match 95.0%; Score 341; DB 4; Length 92;  
Best Local Similarity 97.0%; Pred. No. 7.4e-35;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	KGVSLSPRCPCRFESHVARANKHLINTPCALQIVARLKNRRQVCIDPKLKIOWE 60
DB	22	KVSLSPRCPCRFESHVARANKHLINTPCALQIVARLKNRRQVCIDPKLKIOWE 81
QY	61	YLEKALN 67
DB	82	YLEKALN 88

```

RESULT 2
Q90ZD1 PRELIMINARY; PRT; 89 AA.
AC Q90ZD1:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Stromal cell-derived factor-1 alpha.
GN SDF-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Ohtani Y., Okada M., Kawaguchi N., Minami M., Satoh M.;
RT "CDNA cloning of rat stromal cell-derived factor-1 alpha (SDF-1
alpha).";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Pillariseti K., Gupta S.K.;
RT "Identification and molecular cloning of a novel rat ortholog of the
RT alpha chemokine, stromal cell derived factor-1 (SDF-1).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF189724; AAF01066.1; -
DR EMBL: AF209976; AAG43506.1; -
DR HSSP: P48061; ISDP
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
SQ SEQUENCE 89 AA; 9977 MW; D86977626A2E35FA CRC64;

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```

Query Match 92.8%; Score 333; DB 11; Length 89;
Best Local Similarity 94.0%; Pred. No. 7.1e-34;
Matches 63; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 KGVSLSPRCPCRFESHVARANKYHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 22 KPVSLSYRCPCRFESHVARANKYHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81
QY 61 YLEKALN 67
|:||||
DB 82 YLDKALN 88

```

```

RESULT 3
Q80UJ9 PRELIMINARY; PRT; 94 AA.
AC Q80UJ9:
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Stromal-derived factor 1 precursor.
GN SDF-1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Braun M., Wunderlin M., Knoechel W., Gierschik P., Moepf B.;
RT "Xenopus laevis stromal-derived factor 1: conservation of structure
RT and function during vertebrate development.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: A1278857; CAC82196.1; -
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
KW Signal.

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```

FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 94 STROMAL-DERIVED FACTOR 1.
SO SEQUENCE 94 AA; 10701 MW; 8C8325D152F326E7 CRC64;

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```

Query Match 76.6%; Score 275; DB 13; Length 94;
Best Local Similarity 73.1%; Pred. No. 1.2e-26;
Matches 49; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

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```

QY 1 KGVSLSPRCPCRFESHVARANKYHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 22 KPVSLSYRCPCRFESHVARANKYHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81
QY 61 YLEKALN 67
|:||||
DB 82 YLEKALN 88

```

```

RESULT 4
Q91ZL1 PRELIMINARY; PRT; 91 AA.
AC Q91ZL1:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE RANTES chemokine.
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RA Bianco J.C., Pietneva L.M., Prince G.A.;
RT "Sigmodon hispidus cytokines, chemokines and interferons.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF421591; AAL16932.1; -
DR InterPro: IPR000827; CC_chemkine_sm1.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; UNKNOWN.1.
SQ SEQUENCE 91 AA; 10082 MW; D0D6EABEB4242EF CRC64;

```

```

Query Match 26.3%; Score 94.5; DB 11; Length 91;
Best Local Similarity 37.3%; Pred. No. 0.00032;
Matches 22; Conservative 9; Mismatches 25; Indels 3; Gaps 2;

```

```

QY 6 SPKPCRF--FESHVARANKYHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOEYL 62
| | | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
DB 28 SDTIPCCFAYLSAVLPRAVKEY-FYTSSKCSNFAVFEVRRNRQVCANPKKRWQYEYI 85

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```

RESULT 5
Q80GV8 PRELIMINARY; PRT; 98 AA.
AC Q80GV8:
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CXCL chemokine.
GN CXCL CHEMOKINE.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralicthyidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Aoki T., Hirose I., Lee J., Iwahori A.;
RT "Molecular cloning and expression of IL-1b and two types of chemokines
RT in Japanese flounder, Paralicthys olivaceus.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB070837; BAB86884.1; -

```

```

SQ SEQUENCE 98 AA: 10846 MW: 495CA4839A5DBC92 CRC64:
Query Match 24.5%; Score 88; DB 13; Length 98;
Best Local Similarity 31.9%; Pred. No. 0.0022;
Matches 22; Conservative 17; Mismatches 24; Indels 6; Gaps 4;

OY 2 GVSLSPRCPCFFESHVARANKHLKILINTPN-C-AIQIYARLKNNNRQVCIDPKLKMI 58
    |||| | | | | :|::|: || | | | |::|: || | |
Db 30 GVSL-HCRCLTETESRPGRIGRIKSVEII-SPNSHCDKTEIIATFLKDGVGLCLDPEAPWV 86

OY 59 QEYLEKALN 67
   : | ::
Db 87 KRVINKLIS 95

RESULT 6
O90YV59 PRELIMINARY: PRT; 109 AA.
AC O90YV59:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Interleukine-8.
GN IL-8.
OS Paralicthys olivaceus (Flounder).
OC Euarthropoda; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphia; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralichthyidae; Paralichthys.
OX NCBI_Taxid=8255;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21435923; PubMed=11551708;
RA Lee E.Y., Park H.H., Kim Y.T., Chung J.K., Choi T.J.;
RT "Cloning and sequence analysis of the interleukin-8 gene from flounder
RT (Paralichthys olivaceus).";
RL Gene 274;237-243(2001);
DR EMBL; AF216646; AAL05442.1;
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
SO SEQUENCE 109 AA; 12117 MW; C7CE18986C50A6ED CRC64:

Query Match 24.5%; Score 88; DB 13; Length 109;
Best Local Similarity 31.9%; Pred. No. 0.0025;
Matches 22; Conservative 17; Mismatches 24; Indels 6; Gaps 4;

OY 2 GVSLSPRCPCFFESHVARANKHLKILINTPN-C-AIQIYARLKNNNRQVCIDPKLKMI 58
    |||| | | | | :|::|: || | | | |::|: || | |
Db 29 GVSL-HCRCLTETESRPGRIGRIKSVEII-SPNSHCDKTEIIATFLKDGVGLCLDPEAPWV 85

OY 59 QEYLEKALN 67
   : | ::
Db 86 KRVINKLIS 94

RESULT 7
O9YVA9 PRELIMINARY: PRT; 134 AA.
AC O9YVA9:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE VIL8 (CXc chemokine VIL8).
GN MDV003 OR MDV078.
OS Gallid herpesvirus 1.
OS Marek's disease herpesvirus (strain GA) (MDHV), and
OS Marek's disease herpesvirus (strain Md5) (MDHV), Turkey herpesvirus.
OS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.
NCBI_Taxid=10386, 10388, 10389;
RN [1]
RP SEQUENCE FROM N.A.
RX SPECIES=Gallid herpesvirus 1; STRAIN-RBIB;
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RA Rassaert D., Fragnet L.;
RT "Characterisation of the BmH1 L fragment of the Marek's disease virus
RB strain (serotype 1).";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN 121
RP SEQUENCE FROM N.A.
RC SPECIES=Marek's disease herpesvirus (strain GA) (MDHV);
RA Lin S.-F., Robinson D., Chen H.-C., Kung H.-J.;
RT "CXC chemokine encoded by Marek's Disease Virus (MDV).";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN 131
RP SEQUENCE FROM N.A.
RC SPECIES=Marek's disease herpesvirus (strain Md5) (MDV);
RX MEDLINE=20392152; PubMed=10933706;
RA Tulman E.R., Alfonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
RT "The genome of a very virulent Marek's disease virus.";
RL J. Virol. 74:7980-7988(2000).
RN 141
RP SEQUENCE FROM N.A.
RC SPECIES=Marek's disease herpesvirus (strain Md5) (MDV);
RA Tulman E.R., Alfonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF311499; AAL58097.1; -
DR EMBL: AF065430; AAC77449.1; -
DR EMBL: AF234348; AAG14290.1; -
DR EMBL: AF234348; AAG14256.1; -
DR HSSP: P10889; IMI2.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXC_chemokine_small.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTCKXC.
DR SMART: SM00199; SCV; 1.
SQ SEQUENCE 134 AA; 14828 MW; C859CDB868D25190 CRC64;

Query March 23.5%; Score 84.5; DB 12; Length 134;
Best Local Similarity 25.9%; Pred No. 0.0083;
Matches 22; Conservative 14; Mismatches 12; Indels 37; Gaps

QY 2 GVSL-----SPRCPCRFESHVARANVXKLILNTP-----NC-ALQIV 39
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 22 GISLESLAVDKRKC-----VKYTNPTGCLPIAVDIVPGHCRRETI 67

QY 40 ARKNNRQVCIDPKLKIQIYLEK 64
   || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68 FALK-KNRKVCVDEPAPWQDFIKK 91

RESULT 8
Q9IBJ7 PRELIMINARY; PRT; 142 AA.
AC Q9IBJ7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE VIL-8.
GN R-LORF2.
OS Turkey herpesvirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Marek's disease-like viruses.
CX NCBI_TaxID=10390;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN-GA;
RX MEDLINE=92237304; PubMed=115048;
RA Jones D., Lee L., Liu J.L., Kung H.J., Tiliotson J.K.;
RT "Marek disease virus encodes a basic-leucine zipper gene resembling
RT the fos/jun oncogenes that is highly expressed in lymphoblastoid
RL tumors.";
RN Proc. Natl. Acad. Sci. U.S.A. 89:4042-4046(1992).
RP SEQUENCE FROM N.A.
RC STRAIN-GA;
RA Lee L.F., Wu P., Sul D., Ren D., Kung H.J.;

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RT "The Complete UL Sequence of Serotype I Marek's Disease Virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2000).
DR EMBL: AF147806; AAF67205.1; -.
DR EMBL: AF147806; AAF6793.1; -.
DR HSSP: P10889; 1MI2.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXCL1; Chemokine-sm1.
DR InterPro: IPR001230; Prey1L_site.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTCKXC.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00294; PRENYLATION; UNKNOWN_1.
SQ SEQUENCE 142 AA; 15770 MW; 35ABCEB9B29FD209 CRC64;

Query Match 23.5%; Score 84.5; DB 12; Length 142;
Best Local Similarity 25.9%; Pred. No. 0.0088;
Matches 22; Conservative 14; Mismatches 12; Indels 37; Gaps 5;

QY 2 GVSU-----SPRCPREFESHVARANKHLKILNTP-----NC-ALQIVARLK 39
DB 22 GISLESLAVDRKRC-----YKVTNRPTGLPIAVDVIPGTHCRREI 67
QY 40 ARKNNRQVCIDPKLKWIOEYLEK 64
DB 68 FALK-KNRKVCVDEAPVVOOFIRK 91

RESULT 9
QY 067634 PRELIMINARY; PRT; 203 AA.
AC 067634;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Eco Q protein (Fragment).
OS Marek's disease herpesvirus (strain GA) (MDHV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Marek's disease-like viruses.
OX NCBI_TaxID=10388;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GA;
RX MEDLINE=96074534; PubMed=7491783;
RA Peng Q., Zeng M., Bhuiyan Z.A., Ubukata E., Tanaka A., Nonoyama M.,
RA Shirazi Y.;
RT "Isolation and characterization of Marek's disease virus (MDV) cDNAs
RT mapping to the BamHI-12, BamHI-02, and BamHI-L fragments of the MDV
RT genome from lymphoblastoid cells transformed and persistently infected
RT with MDV.";
RL Virology 213:590-599(1995).
DR EMBL: U34966; AAC54629.1; -.
DR HSSP: P10889; 1MI2.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; CXCL1; Chemokine-sm1.
DR InterPro: IPR004827; TP_BZIP.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTCKXC.
DR SMART: SM00338; BRIZ; 1.
DR SMART: SM00199; SCY; 1.
DR SMART: SM00199; SCY; 1.
FT NON_TER 1
SQ SEQUENCE 203 AA; 23132 MW; DE42F2A1C1A71C88 CRC64;

Query Match 23.4%; Score 84; DB 12; Length 203;
Best Local Similarity 23.5%; Pred. No. 0.015;
Matches 19; Conservative 17; Mismatches 13; Indels 32; Gaps 4;

QY 1 KGVSLSPRCPCREFESHVARANKHLKILNTP-----NC-ALQIVARLK 43
DB 95 ESLAVDRKRC-----YKVTNRPTGLPIAVDVIPGTHCRREI 140
QY 44 NNRQVCIDPKLKWIOEYLEK 64
DB 141 -KNRKCVCVDEAPVVOOFIRK 160

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RESULT 10
QY 080FP5 PRELIMINARY; PRT; 97 AA.
AC 080FP5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CXC chemokine.
CXK CHEMOKINE.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEAD KIDNEY;
RA Savan R., Kono T., Aman A., Sakai M.;
RT "Molecular cloning and analysis of a novel CXC chemokine gene in
RT common carp.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB082985; BAB8677.1; -.
SQ SEQUENCE 97 AA; 10846 MW; 04A1A1F008989535 CRC64;

Query Match 22.7%; Score 81.5; DB 13; Length 97;
Best Local Similarity 31.0%; Pred. No. 0.014;
Matches 22; Conservative 16; Mismatches 28; Indels 5; Gaps 2;

QY 1 KGVSLSPRCPCREFESHVARANKHLK-----INTPNCALQ-IVARLKNRQVCIDPKL 55
DB 19 KGQARARKGCFVCVKVNNVPPKQIKELIPASRCKTQELVYLKSTEQKLNPS 78
QY 56 KWIQEVLEKAL 66
DB 79 KFTQKYMKAIV 89

RESULT 11
QY 098158 PRELIMINARY; PRT; 95 AA.
AC 098158;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUL-1997 (TrEMBLrel. 17, Last annotation update)
DE ORF K6.
OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97094384; PubMed=8939871;
RA Moore P.S., Bashoff C., Weiss R.A., Chang Y.;
RT "Molecular mimicry of human cytokine and cytokine response pathway
RT genes by KSHV.";
RL Science 274:1739-1744(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97121480; PubMed=8962146;
RA Russo J.J., Bohenkky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RT "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
RT (HHV8).";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX Russo J.J., Bohenkky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
SQ SEQUENCE FROM N.A.

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RA Nicholas J., Ruvoletto V.R., Burns W.H., Sandford G., Wan X., Ciuflo D.,  
 RA Hendrickson S., Guo H.C., Hayward G.S., Reitz M.S.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Russo J.D., Bohenzky R.A., Chlen M.C., Chen J., Yan M., Madalena D.,  
 RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-97296220; PubMed-9151804;  
 RA Neipel F., Albrecht J.C., Fleckenstein B.;  
 RT "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus  
 RT human herpesvirus 8: determinants of its pathogenicity?";  
 RL J. Virol. 71:4187-4192(1997).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA Sun R., Lin S.-F., Miller G.;  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RA Ren S., Lin S.-F., Miller G.;  
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U75698; AAC57095.1; -;  
 DR EMBL: U74585; AAB61704.1; -;  
 DR EMBL: U93872; AAB62671.1; -;  
 DR EMBL: U71366; AAC34943.1; -;  
 DR EMBL: U50138; AAD11536.1; -;  
 DR HSSP: Q98157; IYMP.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PF00048; IL8; 1.  
 DR SMART: SM00199; SCY; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 95 AA; 10485 MW; 34B9AFC4987FEC485 CRC64;

Query Match 22.6%; Score 81; DB 12; Length 95;  
 Best Local Similarity 25.8%; Pred. No. 0.016;  
 Matches 16; Conservative 11; Mismatches 35; Indels 0; Gaps 0;  
 Oy 3 VLSLPRCGRFESHVARANKHLKILNTPMCAIQIYARLNKNNRQVCIDPKLKIQEYL 62  
 Db 29 VSYPNSCVGFQOHPPVQILKEWYPTSPACPKPGVILLTRGRQICADPSKNMVRQLM 88  
 Oy 63 EK 64  
 Db 89 QR 90  
 RESULT 12  
 ID 073912 PRELIMINARY; PRT; 104 AA.  
 AC 073912;  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE K60 protein precursor (CXC chemokine K60).  
 CN K60.  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=MACROPHAGE LIKE;  
 RA Slick C.;  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-20170941; PubMed-10704244;  
 RA Slick C., Schneider K., Staeheli P., Wehling K.C.;  
 RT "Novel chicken CXC and CC chemokines.";  
 RL Cytokine 12:181-186(2000).

RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Hughes S.M., Bumstead N.;  
 RT "Mapping of a second EIR CXC chemokine to chicken chromosome four.";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Y14971; CAW5212.1; -;  
 DR EMBL: AF277660; AAF6485.1; -;  
 DR HSSP: P02775; IYVX.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR InterPro: IPR001089; CXC-chemokine-sm1.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS: PR00437; SMALLCYTCXC.  
 DR SMART: SM00199; SCY; 1.  
 DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; 1.  
 KW Signal.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 104 K60 PROTEIN.  
 SQ SEQUENCE 104 AA; 11199 MW; 83725AB91FE18E3D CRC64;

Query Match 22.6%; Score 81; DB 13; Length 104;  
 Best Local Similarity 29.2%; Pred. No. 0.017;  
 Matches 19; Conservative 18; Mismatches 20; Indels 8; Gaps 4;

Oy 8 RCPGRFESHVARANKHLKILNTPMCAIQIYARLNKNNRQVCIDPKLKIQEYL 62  
 Db 33 RQGC--LETHSKFHPRKIQNVNLLPSGPHCKNVEIATLK-DGREVCCLDPTAPVVKLLI 89  
 Oy 63 EKALN 67  
 Db 90 KALID 94

RESULT 13  
 ID 092318 PRELIMINARY; PRT; 97 AA.  
 AC 092318;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Monocyte chemoattractant protein-3 (MCP-3).  
 OS Cavia porcellus (Guinea pig).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Hystriognathli; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LUNG;  
 RA Asano K., Nakamura M., Oguma T., Fukunaga K., Matsubara H.,  
 RA Ishizaka A., Yamaguchi K., Kanazawa M.;  
 RT "Differential expression of CC chemokines in guinea pig lungs during  
 RT an allergic inflammation.";  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB014340; BAA36456.1; -;  
 DR HSSP: P51671; IEOT.  
 DR InterPro: IPR000827; CC-chemokine-sm1.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PF00048; IL8; 1.  
 DR SMART: SM00199; SCY; 1.  
 DR PROSITE: PS00472; SMALL\_CYTOKINES\_CC; 1.  
 SQ SEQUENCE 97 AA; 11159 MW; E1B9A17C165C2421 CRC64;

Query Match 22.1%; Score 79.5; DB 11; Length 97;  
 Best Local Similarity 30.3%; Pred. No. 0.025;  
 Matches 20; Conservative 13; Mismatches 28; Indels 5; Gaps 2;  
 Oy 2 GVSLSRCPGRFESHVARANKHLKILNTPMCAIQIYARLNKNNRQVCIDPKLKIQEYL 60  
 Db 27 GVNISTCCYKRSQRIRVR--LESTRTITSSCKPMQAVIFTKFKREICADPKQQWVDS 84  
 Oy 61 --YLEEK 64  
 Db 85 MKYIDK 90



GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: January 23, 2003, 15:27:48 : Search time 28.2 seconds  
(without alignments)  
316.568 Million cell updates/sec

Title: US-09-852-424-5

Perfect score: 361

Sequence: 1 KGVSLSTYPCPCRFESHVAR.....QVCIDPKLKIOWLEKALN 67

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

A\_Geneseq\_101002:\*

- 1: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:\*
- 2: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:\*
- 3: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:\*
- 4: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:\*
- 5: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:\*
- 6: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:\*
- 7: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:\*
- 8: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:\*
- 9: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:\*
- 10: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:\*
- 11: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:\*
- 12: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:\*
- 13: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:\*
- 14: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:\*
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- 19: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:\*
- 20: /SID2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:\*
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- 22: /SID2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*
- 23: /SID2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	361	100.0	67	23	AA48660
2	352	97.5	67	23	AA48656
3	347	96.1	67	23	AA48658
4	345	95.6	67	23	AA48657
5	344	95.3	67	19	AA50760
6	344	95.3	67	20	AAV34092
7	344	95.3	67	20	AAV06741
8	344	95.3	67	20	AAV06726
9	344	95.3	67	21	AAV67594
10	344	95.3	67	23	AA47680

11	344	95.3	68	19	AA50761
12	344	95.3	69	20	AAV05818
13	344	95.3	72	19	AAV50762
14	344	95.3	72	20	AAV34093
15	344	95.3	72	21	AAV67595
16	344	95.3	73	19	AAV50763
17	344	95.3	73	20	AAV05819
18	344	95.3	74	21	AAV69041
19	344	95.3	89	16	AAV75419
20	344	95.3	89	20	AAV39959
21	344	95.3	89	20	AAV26177
22	344	95.3	89	21	AAV5791
23	344	95.3	89	21	AAV93603
24	344	95.3	89	21	AAV52508
25	344	95.3	90	20	AAV05820
26	344	95.3	93	16	AAV75420
27	344	95.3	93	19	AAV50766
28	344	95.3	93	20	AAV26178
29	344	95.3	93	20	AAV06725
30	344	95.3	93	21	AAV15812
31	344	95.3	93	23	AAE23952
32	344	95.3	93	23	AAU84305
33	344	95.3	93	23	AAV47690
34	344	95.3	93	23	AAV47691
35	344	95.3	94	20	AAV05821
36	344	95.3	101	23	AAV48051
37	344	95.3	119	23	AAV48047
38	344	95.3	166	20	AAV29899
39	344	95.3	177	20	AAV29896
40	344	95.3	320	21	AAV69055
41	344	95.3	322	21	AAV69056
42	344	95.3	326	19	AAV76221
43	344	95.3	327	21	AAV69057
44	344	95.3	328	19	AAV76220
45	344	95.3	339	20	AAV29905

## ALIGNMENTS

## RESULT 1

ID AA48660 standard; peptide; 67 AA.

AA48660;

20-MAY-2002 (first entry)

CXCR4 peptide antagonist SEQ ID NO 5.

CXCR4; haematopoietic cell; chemokine receptor-4; cytostatic; immunosuppressive; cancer; autoimmune disease; peripheral blood locus; cell multiplication.

Synthetic.

Key Location/Qualifiers

Modified-site 8 /note="Optionally the proline analogue 6-amino-7-oxo-2,3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic acid residue"

WO200185196-A2.

15-NOV-2001.

09-MAY-2001; 2001WO-CA00659.

09-MAY-2000; 2000CA-2305787.

19-MAY-2000; 2000US-205467P.

(UVR-) UNIV BRITISH COLUMBIA.  
(CHEM-) CHEMOKINE THERAPEUTICS CORP.

Peptide which bind  
N-terminal modifie  
Peptide which bind  
Native stromal cel  
SDF-beta peptide  
Peptide which bind  
N-terminal modifie  
Amino acid sequenc  
Human SDF-1-alpha.  
Human SDF-1-alpha  
Stromal cell deriv  
Human chemokine SD  
A human B-cell sti  
Human stromal cell  
N-terminal modifie  
Human SDF-1-beta.  
Human SDF-1 which  
Stromal cell deriv  
Amino acid sequenc  
Human chemokine SD  
Human stromal cell  
Human endometrial  
SDF-1 precursor.  
SDF-1-beta. Homo  
N-terminal modifie  
SDF-1gamma SEQ ID  
Human SDF-1gamma S  
Human SDF-1 beta a  
Human SDF1 and hum  
A chemokine recept  
A chemokine recept  
Human chemokine SD  
A chemokine recept  
Human chemokine SD  
Human SDF-1 and hu

XX Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;  
 PI Clark-Lewis I, Salari H;  
 XX  
 XX  
 DR WPI; 2002-106073/14.  
 XX  
 PT Promoting the rate of haematopoietic cell multiplication for treating a  
 PT cancer involves administering chemokine receptor antagonist to the  
 PT cells -  
 XX  
 PS Claim 9; Page 54; 68pp; English.  
 CC The invention relates to a method of promoting the rate of haematopoietic  
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)  
 CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist  
 CC has cytostatic and immunosuppressive activity and is useful for treating  
 CC cancer or autoimmune disease in a patient; to promote the rate of  
 CC haematopoietic cell multiplication; to formulate a medicament for  
 CC increasing the circulation of the haematopoietic cells in a patient; for  
 CC mobilising haematopoietic cells from a narrow locus to a peripheral blood  
 CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The  
 CC CXCR4 antagonists stimulates haematopoietic cell multiplication,  
 CC self-renewal, expansion and proliferation of peripheralisation in vivo.  
 CC  
 XX  
 SQ Sequence 67 AA;  
 Query Match 100.0%; Score 361; DB 23; Length 67;  
 Best Local Similarity 100.0%; Pred. No. 1e-39; Mismatches 0; Gaps 0;  
 Matches 67; Conservative 0; Indels 0;  
 QY 1 KGVSLSTPCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 Db 1 KGVSLSTPCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 QY 61 YLEKALN 67  
 Db 61 YLEKALN 67  
 Db 61 YLEKALN 67  
 RESULT 2  
 AAM48656  
 ID AAM48656 standard; peptide; 67 AA.  
 AC AAM48656;  
 XX  
 DT 20-MAY-2002 (first entry)  
 DE CXCR4 peptide antagonist SEQ ID NO 1.  
 XX  
 DE CXCR4 peptide antagonist SEQ ID NO 1.  
 XX  
 KM CRCX4; haematopoietic cell; chemokine receptor-4; cytostatic;  
 KM immunosuppressive; cancer; autoimmune disease; peripheral blood locus;  
 KM cell multiplication.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200185196-A2.  
 PD 15-NOV-2001.  
 PF 09-MAY-2001; 2001WO-CA00659.  
 PR 09-MAY-2000; 2000CA-2305787.  
 PR 19-MAY-2000; 2000US-205467P.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 XX  
 PI Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;  
 PI Clark-Lewis I, Salari H;  
 XX  
 DR WPI; 2002-106073/14.  
 XX  
 PT Promoting the rate of haematopoietic cell multiplication for treating a

PT cancer involves administering chemokine receptor antagonist to the  
 PT cells -  
 XX  
 XX  
 PS Claim 9; Page 54; 68pp; English.  
 CC The invention relates to a method of promoting the rate of haematopoietic  
 CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)  
 CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist  
 CC has cytostatic and immunosuppressive activity and is useful for treating  
 CC cancer or autoimmune disease in a patient; to promote the rate of  
 CC haematopoietic cell multiplication; to formulate a medicament for  
 CC increasing the circulation of the haematopoietic cells in a patient; for  
 CC mobilising haematopoietic cells from a narrow locus to a peripheral blood  
 CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The  
 CC CXCR4 antagonists stimulates haematopoietic cell multiplication,  
 CC self-renewal, expansion and proliferation of peripheralisation in vivo.  
 CC  
 XX  
 SQ Sequence 67 AA;  
 Query Match 97.5%; Score 352; DB 23; Length 67;  
 Best Local Similarity 98.5%; Pred. No. 1.6e-38; Mismatches 1; Indels 0; Gaps 0;  
 Matches 66; Conservative 0;  
 QY 1 KGVSLSTPCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 Db 1 KGVSLSTPCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 QY 61 YLEKALN 67  
 Db 61 YLEKALN 67  
 Db 61 YLEKALN 67  
 RESULT 3  
 AAM48658  
 ID AAM48658 standard; peptide; 67 AA.  
 AC AAM48658;  
 XX  
 DT 20-MAY-2002 (first entry)  
 DE CXCR4 peptide antagonist SEQ ID NO 3.  
 XX  
 DE CXCR4 peptide antagonist SEQ ID NO 3.  
 XX  
 KM CRCX4; haematopoietic cell; chemokine receptor-4; cytostatic;  
 KM immunosuppressive; cancer; autoimmune disease; peripheral blood locus;  
 KM cell multiplication.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 6 /note= "Optionally the proline analogue 6-amino-7-oxo-2,  
 FT 3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic  
 FT acid residue or a bicyclic turned dipeptide  
 FT (Btd)"  
 XX  
 PN WO200185196-A2.  
 PD 15-NOV-2001.  
 PF 09-MAY-2001; 2001WO-CA00659.  
 PR 09-MAY-2000; 2000CA-2305787.  
 PR 19-MAY-2000; 2000US-205467P.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
 XX  
 PI Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;  
 PI Clark-Lewis I, Salari H;  
 XX  
 DR WPI; 2002-106073/14.  
 XX  
 PT Promoting the rate of haematopoietic cell multiplication for treating a



PT cancer involves administering chemokine receptor antagonist to the  
PT cells -  
XX  
PS Claim 9; Page 54; 68pp; English.  
PS  
XX  
CC The invention relates to a method of promoting the rate of haematopoietic  
CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)  
CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist  
CC has cytostatic and immunosuppressive activity and is useful for treating  
CC cancer or autoimmune disease in a patient; to promote the rate of  
CC haematopoietic cell multiplication; to formulate a medicament for  
CC increasing the circulation of the haematopoietic cells in a patient; for  
CC mobilising haematopoietic cells from a narrow locus to a peripheral blood  
CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The  
CC CXCR4 antagonists stimulates haematopoietic cell multiplication,  
CC self-renewal, expansion and proliferation of peripheralisation in vivo.  
CC  
XX  
SO Sequence 67 AA:  
  
Query Match 96.1%; Score 347; DB 23; Length 67;  
Best Local Similarity 97.0%; Pred. No. 7e-38;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
OY 1 KGVSLSTPCPCFFESHVARANVKHLKILNTPNCALQIYARLKNNNROYCIDPKLKWIOE 60  
Db 1 KGVSLSTPCPCFFESHVARANVKHLKILNTPNCALQIYARLKNNNROYCIDPKLKWIOE 60  
  
OY 61 YLEKALN 67  
Db 61 YLEKALN 67  
  
RESULT 4  
AAM48657  
ID AAM48657 standard; peptide: 67 AA.  
XX  
AC AAM48657:  
XX  
DT 20-MAY-2002 (first entry)  
XX  
DE CXCR4 peptide antagonist SEQ ID NO 2.  
XX  
XX  
XX CRXC4; haematopoietic cell; chemokine receptor-4; cytostatic;  
KW immunosuppressive; cancer; autoimmune disease; peripheral blood locus;  
XX cell multiplication.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FH Modified-site 5 /note="optionally the proline analogue 6-amino-7-oxo-2,  
FT 3,4,5,6,7-hexahydro-1H-indolizine-1-carboxylic  
FT acid residue or a bicyclic turned dipeptide  
FT (Bcd)"  
XX  
PN WO200185196-A2.  
XX  
PD 15-NOV-2001.  
XX  
PE 09-MAY-2001; 2001WO-CA00659.  
XX  
PR 09-MAY-2000; 2000CA-2305787.  
XX  
PR 19-MAY-2000; 2000US-205467P.  
XX  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
XX  
PI Tudan CR, Merzouk A, Arab L, Saxena G, Eaves CJ, Cashman J;  
XX Clark-Lewis I, Salarl H;  
XX  
XX WPI: 2002-106073/14.  
PT Promoting the rate of haematopoietic cell multiplication for treating a

PT cancer involves administering chemokine receptor antagonist to the  
PT cells -  
PS Claim 9; Page 54; 68pp; English.  
XX  
XX  
CC The invention relates to a method of promoting the rate of haematopoietic  
CC cell multiplication comprising administering chemokine receptor-4 (CXCR4)  
CC antagonist (AAM48656-AAM48701) to haematopoietic cells. The antagonist  
CC has cytostatic and immunosuppressive activity and is useful for treating  
CC cancer or autoimmune disease in a patient; to promote the rate of  
CC haematopoietic cell multiplication; to formulate a medicament for  
CC increasing the circulation of the haematopoietic cells in a patient; for  
CC mobilising haematopoietic cells from a narrow locus to a peripheral blood  
CC locus; in the treatment of haematopoietic cells in vitro and in vivo. The  
CC CXCR4 antagonists stimulates haematopoietic cell multiplication,  
CC self-renewal, expansion and proliferation of peripheralisation in vivo.  
CC  
XX  
SQ Sequence 67 AA:  
  
Query Match 95.6%; Score 345; DB 23; Length 67;  
Best Local Similarity 97.0%; Pred. No. 1.3e-37;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 KGVSLSYPCRFESHVARANVKKLTLPNCALQIVARLKNRRVCIIDPKLKWIOE 60  
Db 1 KGVSFSPYRCPCRFESHVARANVKKLTLPNCALQIVARLKNRRVCIIDPKLKWIOE 60  
QY 61 YLEKALN 67  
Db 61 YLEKALN 67  
  
RESULT 5  
AAW50760  
ID AAW50760 standard; peptide: 67 AA.  
XX  
XX AAW50760;  
XX  
DT 27-JUL-1998 (first entry)  
XX  
DE Peptide which binds to CXCR4 receptor and is useful for treating HIV.  
XX  
XX Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus;  
KM HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.  
XX  
XX Homo sapiens.  
OS  
XX FR2751658-A1.  
PN  
XX 30-JAN-1998.  
PD  
XX 26-JUL-1996; 96FR-0009477.  
PF  
XX 26-JUL-1996; 96FR-0009477.  
PR  
XX 26-JUL-1996; 96FR-0009477.  
XX  
PA (INSP ) INST PASTEUR.  
XX  
PI Arenzana SF, Baggiolini M, Clark LI, Moser B, Virelizier JL;  
DR WPI; 1998-123039/12.  
XX  
PT Human stromal cell-derived chemokine, SDF-1 - useful for treating  
XX human immunodeficiency virus infection  
XX  
PS Claim 2; Page 29; 48pp; French.  
XX  
CC The invention relates to peptides which bind to a cellular receptor for  
CC CXCR4 chemokines, namely the CXCR4 receptor (also known as leukocyte-  
CC expressed transmembrane domain receptor), especially where the  
CC peptide is human chemokine SDF-1. The peptide can be used to treat or  
CC prevent HIV infections, optionally together with reverse transcriptase  
CC inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4  
CC receptor antagonists, immunotherapy agents, agents for treating HIV-  
CC

CC associated opportunistic infections and/or other CXK or CC chemokines, especially RANTES, MIP-1 alpha, MIP-1 beta or MCP-1. The peptide can be used to detect anti-SDF-1 antibodies in biological fluids. This CC sequence represents a specifically claimed peptide which binds to the CXCR4 receptor.

XX Sequence 67 AA:

Query Match 95.3%; Score 344; DB 19; Length 67;  
Best Local Similarity 97.0%; Pred. No. 1,7e-37;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KVSLSYPCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
DB 1 KPSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67  
DB 61 YLEKALN 67

RESULT 6  
AAV34092  
ID AAV34092 standard; protein; 67 AA.

XX AAV34092;

DT 29-NOV-1999 (first entry)

DE Native stromal cell derived factor 1 (SDF-1) alpha protein.

XX CXK chemokine receptor 4; CXCR4; antagonist; medicament; T-cell;  
KM Interferon gamma; autoimmune disease; multiple sclerosis; cancer;  
KM angiogenesis; stromal cell derived factor 1; SDF-1.

XX Mammalia.

XX WO947158-A2.

XX 23-SEP-1999.

PF 12-MAR-1999; 99WO-CA00221.

XX 13-MAR-1998; 98CA-2226391.

PR 14-AUG-1998; 98CA-2245224.

XX (UYBR-) UNIV BRITISH COLUMBIA.

PI Clark-Lewis I, Gong J, Duronio V;

DR WPI; 1999-561857/47.

PT Use of CXK chemokine receptor 4 for treating autoimmune disease and cancer

XX Example 1; Fig 1; 71pp; English.

XX The invention relates to the use of a CXK chemokine receptor 4 (CXCR4) antagonist for the manufacture of a medicament for reducing interferon gamma production by T-cells in a mammal. The CXCR4 antagonist can be used to treat or to design a medicament to treat, an autoimmune disease, multiple sclerosis, cancer, or for inhibiting angiogenesis. The CXCR4 antagonists may be peptide compounds comprising a substantially purified peptide fragment, analogue or a pharmacologically acceptable salt of stromal cell derived factor 1 (SDF-1). The present sequence represents the amino acid sequence of SDF-1 alpha protein.

XX Sequence 67 AA;

Query Match 95.3%; Score 344; DB 20; Length 67;  
Best Local Similarity 97.0%; Pred. No. 1,7e-37;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KVSLSYPCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
DB 1 KPSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67  
DB 61 YLEKALN 67

RESULT 7  
AAV06741  
ID AAV06741 standard; protein; 67 AA.

XX AAV06741;

DT 18-JUN-1999 (first entry)

DE SDF-1 alpha/RANTES cross-over chemokine control molecule SSSS.

XX Chemokine; cross-over protein; pharmaceutical; inflammatory; AIDS; viral;  
KM infectious disease; hematopoiesis; chemoprotection; asthma; RANTES; VMP;  
KM allergic rhinitis; atopic dermatitis; rheumatoid arthritis; SDF-1; MPV;  
KM stromal cell derived factor 1; Macrophage inflammatory protein.

XX Synthetic.

OS Homo sapiens.

PN WO9911655-A1.

PD 11-MAR-1999.

PF 31-AUG-1998; 98WO-US18096.

PR 04-SEP-1997; 97US-0057620.

XX (GRYP-) GRYPHON SCI.

PA Kent SBH, Siani MA, Simon R, Wilken J;

DR WPI; 1999-205128/17.

PT New cross-over proteins for treatment of inflammation and infections  
e.g. AIDS - prepared by ligation of two functional protein modules  
derived from two different parent molecules

XX Example 4; Page 43; 75pp; English.

XX The invention relates to a cross-over protein produced by chemical ligation of at least two functional protein modules derived from at least two parent protein molecules. The cross-over proteins can be used in pharmaceutical compositions for therapy of inflammatory and infectious diseases including AIDS, and for indications of hematopoiesis and chemoprotection. They are also useful for treatment of asthma, allergic rhinitis, atopic dermatitis and rheumatoid arthritis. A library comprising a collection of cross-over proteins is useful for screening for cross-over proteins that are receptor ligands. The libraries comprise functionally diverse compounds therefore improving the drug discovery process. The proteins and libraries are exemplified by the preparation of cross-over chemokines comprising various combinations of peptide segments derived from RANTES, SDF-1 (stromal cell derived factor 1), VMP (viral Macrophage inflammatory protein) and other such chemokines. Sequences AAV06741-62 represent amino acid sequences of SDF-1 alpha/RANTES cross-over molecules.

XX Sequence 67 AA;

Query Match 95.3%; Score 344; DB 20; Length 67;  
Best Local Similarity 97.0%; Pred. No. 1,7e-37;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KVSLSYPCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
DB 1 KPSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67  
|||||||  
DB 61 YLEKALN 67

RESULT 8  
AAV06726  
ID AAV06726 standard; protein; 67 AA.

XX AAV06726;

DT 18-JUN-1999 (first entry)

XX Amino acid fragment of SDF-1 alpha.

XX Chemokine: cross-over protein; pharmaceutical; inflammatory; AIDS; viral;  
KW infectious disease; hematopoiesis; chemoprotection; asthma; RANTES; vMIP;  
KW allergic rhinitis; atopic dermatitis; rheumatoid arthritis; SDF-1; MPVAV;  
KW stromal cell derived factor 1; Macrophage Inflammatory protein.

OS Homo sapiens.  
OS Synthetic.

PN WO9911655-A1.

PD 11-MAR-1999.

XX 31-AUG-1998: 98WO-US18096.

PR 04-SEP-1997: 97US-0057620.

XX (GRYP-) GRYPHON SCI.

PI Kent SBH, Stanl MA, Simon R, Wilken J;

DR WPI: 1999-205128/17.

XX New cross-over proteins for treatment of inflammation and infections  
PT e.g. AIDS - prepared by ligation of two functional protein modules  
PT derived from two different parent molecules

XX Example 4: Page 41: 75pp: English.

XX The invention relates to a cross-over protein produced by chemical  
CC ligation of at least two functional protein modules derived from at least  
CC two parent protein molecules. The cross-over proteins can be used in  
CC pharmaceutical compositions for therapy of inflammatory and infectious  
CC diseases including AIDS, and for indications of hematopoiesis and  
CC chemoprotection. They are also useful for treatment of asthma, allergic  
CC rhinitis, atopic dermatitis and rheumatoid arthritis. A library  
CC comprising a collection of cross-over proteins is useful for screening  
CC for cross-over proteins that are receptor ligands. The libraries comprise  
CC functionally diverse compounds therefore improving the drug discovery  
CC process. The proteins and libraries are exemplified by the preparation  
CC of cross-over chemokines comprising various combinations of peptide  
CC segments derived from RANTES, SDF-1 (stromal cell derived factor 1), vMIP  
CC (viral Macrophage Inflammatory protein) and other such chemokines. The  
CC present sequence represents an amino acid fragment of SDF-1 alpha which  
CC acts as a synthetic base molecule for synthesizing the cross-over  
CC protein.

XX Sequence 67 AA:

Query Match 95.3%; Score 344: DB 20; Length 67;  
Best Local Similarity 97.0%; Pred. No. 1.7e-37;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLSTPCPCRFEEHVAVRANKHLKILNTPCALSQIVARLKNNNRQVCIDPKLKWIOE 60  
DB 1 KPVSLSTPCPCRFEEHVAVRANKHLKILNTPCALSQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67

DB 61 YLEKALN 67  
|||||||

RESULT 9  
AAV67594  
ID AAV67594 standard; peptide; 67 AA.

XX AAV67594;

DT 13-JUN-2000 (first entry)

XX SDF-1alpha peptide sequence.

XX SDF-1; CXCR4; CXCR chemokine receptor 4; gamma-interferon; cancer; gout;  
KW autoimmune disease; multiple sclerosis; rheumatoid arthritis; psoriasis;  
KW type 1 diabetes; ulcerative colitis; lupus; antagonist; antitumour;  
KW stromal cell derived factor one; anti-inflammatory; immunomodulatory.

XX Unidentified.

PN WO200009152-A1.

PD 24-FEB-2000.

XX 16-AUG-1999: 99WO-CA00750.

PR 14-AUG-1998: 98CA-2245224.

PA (UYBR-) UNIV BRITISH COLUMBIA.

PI Clark-Lewis I, Gong J, Duronio V, Salari H;

DR WPI: 2000-224175/19.

XX Therapeutic composition containing CXCR4 antagonist, useful for  
PT treating autoimmune disease, especially multiple sclerosis and cancer  
PT -

XX Disclosure: Fig 1: 88pp: English.

XX The invention provides a therapeutic composition containing an antagonist  
CC of CXCR4 (CXCR chemokine receptor 4) and an excipient. The compositions  
CC are specifically used: to reduce production of gamma-interferon by T  
CC cells, particularly for treating autoimmune disease, especially multiple  
CC sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral  
CC sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative  
CC colitis, gout, lupus and transplant rejection; to treat cancer by  
CC inhibiting angiogenesis; inhibition of restenosis; and when labeled, to  
CC evaluate in vivo pharmacokinetics, or to determine disease progression  
CC and susceptibility, or as targeting agents for delivery of other  
CC therapeutic agents. The antagonist is selected from SDF-1 (stromal cell  
CC derived factor one) peptide fragments, SDF-1 being the only known natural  
CC ligand for CXCR4. The present sequence represents a SDF-1alpha  
CC peptide sequence.

XX Sequence 67 AA:

Query Match 95.3%; Score 344: DB 21; Length 67;  
Best Local Similarity 97.0%; Pred. No. 1.7e-37;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLSTPCPCRFEEHVAVRANKHLKILNTPCALSQIVARLKNNNRQVCIDPKLKWIOE 60  
DB 1 KPVSLSTPCPCRFEEHVAVRANKHLKILNTPCALSQIVARLKNNNRQVCIDPKLKWIOE 60

OY 61 YLEKALN 67  
DB 61 YLEKALN 67

RESULT 10  
AAB47680

ID AAB47680 standard; peptide: 67 AA.  
XX  
AC AAB47680;  
XX  
DE 30-JAN-2002 (first entry)  
XX  
DE SDF-1-alpha.  
XX  
KW Hematopoietic cell; multiplication; CXCR4 chemokine receptor 4; CXCR4;  
KW agonist; stromal cell derived factor one; SDF-1; autoimmune disease;  
KW macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer;  
KW autologous; allogenic; bone marrow; stem cell; transplantation.  
XX  
OS Homo sapiens.  
XX  
PN WO200176615-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 12-APR-2001; 2001MO-CA00540.  
XX  
PR 12-APR-2000; 2000CA-2305036.  
PR 14-SEP-2000; 2000US-232425P.  
PR 23-FEB-2001; 2001CA-2335109.  
XX  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.  
XX  
PI Salari H, Merzouk A, Arab L, Tudan CR, Saxena G, Eaves CJ;  
PI Cashman J, Clark-Lewis I;  
XX  
DR WPI; 2002-025882/03.  
XX  
PT CXCR4 receptor 4 agonists that reduces hematopoietic cell multiplication  
PT and susceptibility to cytotoxic agents, are useful for bone marrow or  
PT peripheral blood stem cell transplantation  
XX  
PS Claim 8; Page 57; 74pp; English.  
XX  
CC The sequences given in AAB47680-717 represent peptides which may be  
CC used in the method of the invention for reducing the rate of  
CC hematopoietic cell multiplication. These peptides act as CXCR4 chemokine  
CC receptor 4 (CXCR4) agonists to the cells. These peptides are based on  
CC stromal cell derived factor one (SDF-1) with some also containing  
CC sequences derived from macrophage inflammatory protein 1-alpha  
CC (MIP-1-alpha). They can be used to reduce susceptibility of  
CC hematopoietic cells to a cytotoxic agent, by administering one of the  
CC agonist peptides to the cells prior to or during exposure of the  
CC cells to the cytotoxic agent. The CXCR4 agonist is used to reduce  
CC susceptibility of hematopoietic cells to a cytotoxic agent, particularly  
CC in a patient with cancer requiring autologous or allogenic bone marrow  
CC or peripheral blood stem cell transplantation, or an autoimmune disease.  
XX  
SQ Sequence 67 AA;  
XX  
Query Match 95.3%; Score 344; DB 23; Length 67;  
Best Local Similarity 97.0%; Pred. No. 1.7e-37;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSYPCPCRFESHVARANVKKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
ID 1 KPVSLSYRCPCRFESHVARANVKKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
XX  
QY 61 YLEKALN 67  
DE 61 YLEKALN 67  
XX  
Db 61 YLEKALN 67  
XX  
RESULT 11  
ID AAM50761 standard; peptide: 68 AA.  
XX  
AC AAM50761;  
XX

XX  
DT 27-JUL-1998 (first entry)  
XX  
DE Peptide which binds to CXCR4 receptor and is useful for treating HIV.  
XX  
KW Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus;  
KW HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.  
XX  
OS Homo sapiens.  
XX  
PN FR2751658-A1.  
XX  
PD 30-JAN-1998.  
XX  
PF 26-JUL-1996; 96FR-0009477.  
XX  
PR 26-JUL-1996; 96FR-0009477.  
XX  
PA (INSP) INST PASTEUR.  
XX  
PI Arenzana SF, Baggiolini M, Clark LI, Moser B, Virelizier JL;  
XX  
DR WPI; 1998-123039/12.  
XX  
PT Human stromal cell-derived chemokine, SDF-1 - useful for treating  
PT human immunodeficiency virus infection  
XX  
PS Claim 5; Page 29; 48pp; French.  
XX  
CC The invention relates to peptides which bind to a cellular receptor for  
CC CXCR4 chemokines, namely the CXCR4 receptor (also known as leukocyte-  
CC expressed transmembrane domain receptor), especially where the  
CC peptide is human chemokine SDF-1. The peptide can be used to treat or  
CC prevent HIV infections, optionally together with reverse transcriptase  
CC inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4  
CC receptor antagonists, immunotherapy agents, agents for treating HIV-  
CC associated opportunistic infections and/or other CXCR4 or CC chemokines,  
CC especially RANTES, MIP-1-alpha, MIP-1-beta or MCP-1. The peptide can be  
CC used to detect anti-SDF-1 antibodies in biological fluids. This  
CC sequence represents a specifically claimed peptide which binds to the  
CC CXCR4 receptor.  
XX  
SQ Sequence 68 AA;  
XX  
Query Match 95.3%; Score 344; DB 19; Length 68;  
Best Local Similarity 97.0%; Pred. No. 1.8e-37;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSYPCPCRFESHVARANVKKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
ID 2 KPVSLSYRCPCRFESHVARANVKKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 61  
XX  
QY 61 YLEKALN 67  
DE 61 YLEKALN 67  
XX  
Db 62 YLEKALN 68  
XX  
RESULT 12  
ID AAY05818 standard; Protein: 69 AA.  
XX  
AC AAY05818;  
XX  
DT 02-AUG-1999 (first entry)  
XX  
DE N-terminal modified chemokine met-hsDF-1 alpha.  
XX  
KW Stromal cell-derived factor 1 alpha; SDF-1 alpha; met-hsDF-1 alpha;  
KW human; protein engineering; amino-terminal modification; mutant;  
KW HIV; infection; angiogenesis; autoimmune disease; inflammation;  
KW antiangiogenic; antiinflammatory; immunosuppressive; therapy;  
XX  
vaccine.  
XX

OS Homo sapiens.  
 OS Synthetic.  
 PN MO9920759-A1.  
 PD 29-APR-1999.  
 XX  
 XX 21-OCT-1998; 98WO-US22282.  
 PF  
 PR 20-OCT-1998; 98US-0175713.  
 PR 22-OCT-1997; 97US-0955826.  
 PR 27-FEB-1998; 98WO-US04002.  
 XX  
 XX (GENY ) GENETICS INST INC.  
 PA  
 PI Herrmann SH, Lu Z, McCoy JM, Swanberg SL, Walker B;  
 PI Yang O;  
 XX WPI: 1999-288307/24.  
 DR N-PSDB: AAX25530.  
 XX  
 XX Modified chemokines useful for inhibiting or stimulating  
 PT angiogenesis  
 PS  
 PS Claim 6c: Page 79; 85pp; English.  
 XX  
 XX The present sequence represents met-hsdf-1 alpha, i.e. human  
 CC stromal cell derived growth factor-1 alpha having an added  
 CC N-terminal methionine residue. DNA encoding met-hsdf-1 alpha (see  
 CC AA25530) was produced by cloning an NdeI/XbaI-restricted hsdF-1  
 CC alpha PCR product into the E. coli expression vector pAL781  
 CC in-frame with an ATG codon. met-hsdf-1 alpha is an example of  
 CC novel N-terminal modified chemokines (see AA05818-21) that have at  
 CC least one Met residue, at least one aminoxy-pentane residue or at  
 CC least one GroHEK peptide (see AA05822) covalently attached at the  
 CC N-terminus. The N-terminal modified chemokines are useful for  
 CC altering receptor function, inhibiting interactions between  
 CC chemokine receptors and their ligands. They are used as research  
 CC tools for identifying chemokine receptors, as vaccine adjuvants, as  
 CC agents for the chemotactic recruitment of migratory cells, as agents  
 CC for the stimulation or inhibition of angiogenesis, as agents against  
 CC autoimmune diseases and inflammation, and as agents to inhibit the  
 CC binding of HIV to certain receptors and the infection of  
 CC susceptible cells by HIV. HIV infection is best treated with  
 CC modified SDF-1 alpha and beta or MIP-1 alpha and beta.  
 CC  
 XX Sequence 69 AA:  
 SO  
 Query Match 95.3%; Score 344; DB 20; Length 69;  
 Best Local Similarity 97.0%; Pred. No. 1.8e-37;  
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLSTPCPCRFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 DB 2 KPVSLSTPCPCRFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 61  
 OY 61 YLEKALN 67  
 DB 62 YLEKALN 68  
 DB  
 RESULT 13  
 AAWS0762  
 ID AAWS0762 standard; peptide: 72 AA.  
 AC  
 XX AAW50762;  
 AC  
 XX  
 DT 27-JUL-1998 (first entry)  
 XX  
 DE Peptide which binds to CXCR4 receptor and is useful for treating HIV.  
 XX Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus;  
 KW HIV; CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.

XX Homo sapiens.  
 OS  
 OS FR2751658-A1.  
 PN  
 PD 30-JAN-1998.  
 XX  
 XX 26-JUL-1996; 96FR-0009477.  
 PF  
 PR 26-JUL-1996; 96FR-0009477.  
 PR  
 PA (INSP ) INST PASTEUR.  
 PA  
 PI Arenzana SE, Baggiolini M, Clark LI, Moser B, Virelizier JL;  
 PI WPI: 1998-123039/12.  
 DR  
 XX  
 XX Human stromal cell-derived chemokine, SDF-1 - useful for treating  
 PT human immunodeficiency virus infection  
 PT  
 PS Claim 5: Page 29; 48pp; French.  
 XX  
 XX The invention relates to peptides which bind to a cellular receptor for  
 CC CXCR4 chemokines, namely the CXCR4 receptor (also known as leukocyte-  
 CC expressed transmembrane domain receptor), especially where the  
 CC peptide is human chemokine SDF-1. The peptide can be used to treat or  
 CC prevent HIV infections, optionally together with reverse transcriptase  
 CC inhibitors, viral protease inhibitors, soluble CD4 receptors, CD4  
 CC receptor antagonists, immunotherapy agents, agents for treating HIV-  
 CC associated opportunistic infections and/or other CXCR4 or CC chemokines,  
 CC especially RANTES, MIP-1 alpha, MIP-1 beta or MCP-1. The peptide can be  
 CC used to detect anti-SDF-1 antibodies in biological fluids. This  
 CC sequence represents a specifically claimed peptide which binds to the  
 CC CXCR4 receptor.  
 CC  
 XX Sequence 72 AA:  
 SO  
 Query Match 95.3%; Score 344; DB 19; Length 72;  
 Best Local Similarity 97.0%; Pred. No. 1.9e-37;  
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLSTPCPCRFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 DB 1 KPVSLSTPCPCRFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 OY 61 YLEKALN 67  
 DB 61 YLEKALN 67  
 DB  
 RESULT 14  
 AAY34093  
 ID AAY34093 standard; protein: 72 AA.  
 AC  
 XX AAY34093;  
 AC  
 XX  
 DT 29-NOV-1999 (first entry)  
 XX  
 DE Native stromal cell derived factor 1 (SDF-1) beta protein.  
 XX  
 DE CXCR4 chemokine receptor 4; CXCR4; antagonist; medicament; T-cell;  
 KW interferon gamma; autoimmune disease; multiple sclerosis; cancer;  
 KW angiogenesis; stromal cell derived factor 1; SDF-1.  
 XX  
 OS Mammalia.  
 OS  
 PN WO9947158-A2.  
 PN  
 PD 23-SEP-1999.  
 PD  
 PF 12-MAR-1999; 99WO-CA00221.  
 PF  
 XX 13-MAR-1998; 98CA-2226391.

[illegible]

p5		Disclosure; Fig 1; 88pp; English.
xx		
cc	The invention provides a therapeutic composition containing an antagonist	
cc	of CXCR4 (CXc chemokine receptor 4) and an excipient. The compositions	
cc	are specifically used: to reduce production of gamma-interferon by T	
cc	cells, particularly for treating autoimmune disease, especially multiple	
cc	sclerosis but also e.g. Guillain-Barre syndrome, amyotrophic lateral	
cc	sclerosis, rheumatoid arthritis, psoriasis, type 1 diabetes, ulcerative	
cc	colitis, gout, lupus and transplant rejection; to treat cancer by	
cc	inhibiting angiogenesis; inhibition of restenosis; and when labeled, to	
cc	evaluate in vivo pharmacokinetics, or to determine disease progression	
cc	and susceptibility, or as targeting agents for delivery of other	
cc	therapeutic agents. The antagonist is selected from SDF-1 (stromal cell	
cc	derived factor one) peptide fragments, SDF-1 being the only known natural	
cc	ligand for CXCR4. The present sequence represents a SDF-1beta	
cc	peptide sequence.	
xx		
50	Sequence 72 AA:	
	Query Match	95.3%; Score 344; DB 21; Length 72;
	Best Local Similarity	97.0%; Pred. No. 1.9e-37;
	Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0	
QY	1 KGVSLSTPCPCFEFFSHVARANVKKHLKILINTNCALQIYAARKLNKNRQVCIDPKKLWIDE 60   	
Dd	1 KPVSLSYCPCCFEEFSHVAVRANVKKHLKITNTNCALQIYARLKNNNRQCIDPKKLWIDE 60   	
OY	61 YLEKALN 67   	
Dd	61 YLEKALN 67	

Search completed: January 23, 2003, 15:33:43  
Job time : 28.2 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:33:47 : Search time 9.8 Seconds  
(without alignments)  
201.157 Million cell updates/sec

Title: US-09-852-424-5

Perfect score: 361

Sequence: 1 KGVSLSTPCPCRFESHVAR.....QVCIDPKLKWIDELEKALN 67

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents-NA:

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCITUS.COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	344	95.3	89	1	US-08-323-084A-1
2	344	95.3	89	1	US-08-674-008-1
3	344	95.3	93	1	US-08-323-084A-5
4	344	95.3	93	1	US-08-674-008-5
5	344	95.3	326	3	US-08-808-720-3
6	344	95.3	328	3	US-08-808-720-1
7	343	95.0	89	1	US-08-181-556-2
8	93.5	25.9	70	1	US-08-330-163-24
9	93.5	25.9	70	1	US-08-482-111-24
10	93.5	25.9	91	2	US-08-633-682-5
11	93.5	25.9	91	3	US-08-936-772-5
12	93.5	25.9	91	4	US-09-395-918-5
13	93.5	25.9	91	4	US-08-679-493A-156
14	91	25.2	71	3	US-08-615-232A-8
15	91	25.2	71	3	US-08-470-323-8
16	90.5	25.1	66	1	US-08-244-702-13
17	90.5	25.1	67	1	US-08-244-702-12
18	90.5	25.1	67	1	US-08-244-702-14
19	90.5	25.1	68	1	US-08-244-702-9
20	90.5	25.1	68	1	US-08-244-702-10
21	90.5	25.1	68	1	US-08-244-702-11
22	90.5	25.1	69	1	US-08-244-702-2
23	90.5	25.1	69	1	US-08-244-702-3
24	90.5	25.1	69	1	US-08-244-702-4
25	90.5	25.1	69	1	US-08-244-702-5
26	90.5	25.1	69	1	US-08-244-702-6
27	90.5	25.1	69	1	US-08-244-702-7

28	90.5	25.1	69	1	US-08-244-702-8	Sequence 8, Appl
29	90.5	25.1	72	1	US-07-956-863-1	Sequence 1, Appl
30	90.5	25.1	72	1	US-07-778-413E-16	Sequence 16, Appl
31	90.5	25.1	72	1	US-08-340-102-16	Sequence 16, Appl
32	90.5	25.1	72	1	US-08-330-163-1	Sequence 1, Appl
33	90.5	25.1	72	1	US-08-330-163-16	Sequence 16, Appl
34	90.5	25.1	72	1	US-08-244-702-1	Sequence 1, Appl
35	90.5	25.1	72	1	US-08-482-111-1	Sequence 1, Appl
36	90.5	25.1	72	1	US-08-482-111-16	Sequence 16, Appl
37	90.5	25.1	72	1	US-08-482-111-47	Sequence 47, Appl
38	90.5	25.1	72	1	US-08-482-111-49	Sequence 49, Appl
39	90.5	25.1	72	1	US-08-202-989-1	Sequence 1, Appl
40	90.5	25.1	72	5	PCR-US94-02051-1	Sequence 1, Appl
41	90.5	25.1	73	1	US-08-482-111-63	Sequence 63, Appl
42	90.5	25.1	73	1	US-08-482-111-65	Sequence 65, Appl
43	90.5	25.1	73	1	US-08-482-111-69	Sequence 69, Appl
44	90.5	25.1	73	1	US-08-482-111-70	Sequence 70, Appl
45	90.5	25.1	73	4	US-09-384-302A-26	Sequence 26, Appl

## ALIGNMENTS

RESULT 1  
US-08-323-084A-1  
Sequence 1, Application US/08323084A  
Patent No. 5563048  
GENERAL INFORMATION:  
APPLICANT: HONJO, TASUKU  
APPLICANT: SHIROZU, MICHIO  
APPLICANT: TADA, HIDEAKI  
TITLE OF INVENTION: No. 5563048e1 Polypeptides and DNAs encoding them  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SUGHRUE, MIOM, ZINN, MACPEAK & SEAS  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/323,084A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 280505/1993  
FILING DATE: 14-OCT-1993  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 89 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-323-084A-1  
Query Match  
Best local similarity 95.3%; Score 344; DB 1; Length 89;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSTPCPCRFESHVARANKHLKILNTPCALQIVARLKNRRQVCIDPKLKWIDE 60  
Db 22 KPVSLSTPCPCRFESHVARANKHLKILNTPCALQIVARLKNRRQVCIDPKLKWIDE 81  
QY 61 YLEKALN 67









	Matches	20: Conservative	16: Mismatches	21: Indels	3: Gaps
QY	9	CRCRFESHVARANKHLILNT-PNC-ALQIVARLKNRRVOCIDPKLKWIOEYLEKAL	66		
		: : : :           : : : :			
Db	10	CLCKVTSQVAPRHNTLSLEVIKAGRHCTADILALTK-NGRKLCLDPENMKWKIIITKL	68		

RESULT 10  
US-08-633-682-5

```

Sequence 5, Application US/08633682
Patent No. 5840544

GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL RANTES HOMOLOG FROM PROSTATE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,682
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0063 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: GI 475206

```

	25.9%	Score 93.5:	DB 2:	Length 91;
Query Match				
Best Local Similarity	34.5%:	Pred. No.	4e-05;	
Matches	19:	Conservative	10:	Mismatches 25; Indels 1; Gaps 1.
OY	8	PCPCRFESHAVARANKHLKLTNPNCALQIYARIKKNNROYCIDPKIKWIOEYL	62	
	11	11::111	11::111	
	32	PCCEAYISLAPRAHVKEY-EYTSSCKCNLAWEFTRRNRRGCADEPKKWIOEI	85	

RESULT 11  
US-08-936-772-5  
Sequence 5, Application US/08936772  
Patent No. 6015883  
GENERAL INFORMATION:  
APPLICANT: Hawkins, Phillip R.  
BANDMAN, Olga  
APPLICANT: Murry, Lynn E.  
TITLE OF INVENTION: NOVEL RANTES HOMOLOG FROM PROSTATE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive

CITY: Palo Alto  
 STATE: CA  
 COUNTRY: U.S.  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEO Version 1.5  
 CURRENT APPLICATION DATA  
 APPLICATION NUMBER: US/08/936,772  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/633,682  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Luther, Barbara J  
 REGISTRATION NUMBER: 33,954  
 REFERENCE/DOCKET NUMBER: PF-0063 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-852-0195  
 INFORMATION FOR SEQ. ID NO.: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 91 amino acids  
 type: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: GI 45206  
 US-08-936-772-5

## US-08-936-772-5

Query Match	25.9%	Score	93.5	DB	3	Length	91
Best Local	34.5%	Pred.	No.4e-05				
Matches	19	Conservative	10	Mismatches	25	Indels	1
						Gaps	1

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Qy 8 PCPCRFESHVARAVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLWIOEYL 62
   | : | | | : | : | | | : | : | | | :
Db 32 PCCEAYLSLALPRAHKEY - FYTSSKCSNLAVVFYTRNRQVCANPEKKWQOEYI 85
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RESULT 12  
HS-09-395

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US-09-395-918--5
: Sequence 5, Application US/09395918
: Patent No. 6238666
:
: GENERAL INFORMATION:
:
: APPLICANT: Hawkins, Phillip R.
:
: APPLICANT: Bandman, Olga
:
: APPLICANT: Murry, Lynn E.
:
: TITLE OF INVENTION: DNA ENCODING RANTES HOMOLOG FROM PROSTATE
:
: FILE REFERENCE: PF-0063 US
:
: CURRENT APPLICATION NUMBER: US/09/395,918
:
: CURRENT FILING DATE: 1999-09-14
:
: NUMBER OF SEQ ID NOS: 5
:
: SOFTWARE: PERL Program
:
: SEQ ID NO 5
:
: LENGTH: 91
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
:
: FEATURE:
:
: NAME/KEY: misc_feature
:
: OTHER INFORMATION: GenBank: GI 475206
:
: US-09-395-918--5

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	Query Match	25.9%	Score 93.5:	DB 4,	length 91;
	Best Local Similarity	34.5%*	Pred. No.	4e-05;	
	Matches    19; Conservative	10;	mismatches	25;	Indels     1;
	Gaps				1;
Oy	8 PCPCPFESHVARANVKHLKILINPNCALQIVARLKNNNROYCIDPKLKIQEYL	62			
	:::  :	:	::  ::  :	:   ::  :	
b	32 PCCFAYLSIALDPRAHKEY - FYTSSGSKNLAVFTYRRRRCVAPDEKKWQEYI	85			

RESULT 13  
US-08-679-493A-156  
Sequence 156, Application US/08679493A  
Patent No. 6303295  
GENERAL INFORMATION:  
APPLICANT: Taylor, Ethan W.  
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS  
FILE REFERENCE: 55-95  
CURRENT APPLICATION NUMBER: US/08/679,493A  
CURRENT FILING DATE: 1996-07-12  
PRIOR APPLICATION NUMBER: 60/001203  
PRIOR FILING DATE: 1995-07-14  
PRIOR APPLICATION NUMBER: 60/003,112  
PRIOR FILING DATE: 1995-09-01  
NUMBER OF SEQ ID NOS: 216  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 156  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Mus sp.  
US-08-679-493A-156

Query Match  
Best Local Similarity 25.9%; Score 93.5; DB 4; Length 91;  
Best Local Similarity 34.5%; Pred. No. 4e-05;  
Matches 19; Conservative 10; Mismatches 25; Indels 1; Gaps 1;

OY 8 PCPCRFESHVARANKHLKILTPNCALQIYARLKNNNROYCIDPKLWIDLEYL 62  
DB 32 PCCFAYLSIALPRAHKEY-FYTSKSCSNLAVYFTRRRQVCANDEKRWVDYI 85

RESULT 14  
US-08-615-232A-8  
Sequence 8, Application US/08615232A  
Patent No. 5993814  
GENERAL INFORMATION:  
APPLICANT: WILLIAMS, TIMOTHY J.  
APPLICANT: JOSE, PETER J.  
APPLICANT: GRIFFITHS-JOHNSON, DAVID A.  
APPLICANT: HSUAN, JOHN J.  
TITLE OF INVENTION: CHEMOTACTIC CYTOKINE  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/615,232A  
FILING DATE: 13-AUG-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9318984  
FILING DATE: 14-SEP-1993  
APPLICATION NUMBER: GB 9408602  
FILING DATE: 29-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 550-32  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:  
LENGTH: 71 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-615-232A-8

Query Match  
Best Local Similarity 25.2%; Score 91; DB 2; Length 71;  
Best Local Similarity 29.8%; Pred. No. 6.4e-05;  
Matches 17; Conservative 10; Mismatches 30; Indels 0; Gaps 0;

OY 8 PCPCRFESHVARANKHLKILTPNCALQIYARLKNNNROYCIDPKLWIDLEYL 64  
DB 5 PTCCTFFNKQIPLKRVKGYERITSSRCPOEAVIFRTLKNKEVCADPTOKWVDYIAK 61

RESULT 15  
US-08-470-323-8  
Sequence 8, Application US/08470323A  
Patent No. 6031080  
GENERAL INFORMATION:  
APPLICANT: WILLIAMS, TIMOTHY J.  
APPLICANT: JOSE, PETER J.  
APPLICANT: GRIFFITHS-JOHNSON, DAVID A.  
APPLICANT: HSUAN, JOHN J.  
TITLE OF INVENTION: CHEMOTACTIC CYTOKINE  
FILE REFERENCE: 550-33  
CURRENT APPLICATION NUMBER: US/08/470,323A  
CURRENT FILING DATE: 1995-06-06  
EARLIER APPLICATION NUMBER: PCT/GB94/02006  
EARLIER FILING DATE: 1994-09-14  
EARLIER APPLICATION NUMBER: GB 9318984.3  
EARLIER FILING DATE: 1993-09-14  
EARLIER APPLICATION NUMBER: GB 94086902.2  
EARLIER FILING DATE: 1994-04-29  
NUMBER OF SEQ ID NOS: 11  
SEQ ID NO: 8  
LENGTH: 71  
TYPE: PRT  
ORGANISM: guinea pig  
US-08-470-323-8

Query Match  
Best Local Similarity 25.2%; Score 91; DB 3; Length 71;  
Best Local Similarity 29.8%; Pred. No. 6.4e-05;  
Matches 17; Conservative 10; Mismatches 30; Indels 0; Gaps 0;

OY 8 PCPCRFESHVARANKHLKILTPNCALQIYARLKNNNROYCIDPKLWIDLEYL 64  
DB 5 PTCCTFFNKQIPLKRVKGYERITSSRCPOEAVIFRTLKNKEVCADPTOKWVDYIAK 61

Search completed: January 23, 2003, 15:38:59  
Job time : 10.8 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:31:18 : Search time 6.2 seconds  
(without alignments)  
218.059 Million cell updates/sec

Title: US-09-852-424-5  
Perfect score: 361  
Sequence: 1 KGVSLSTPCPCRFESHVAR.....QVCIDPKIKIQLYLEKALN 67

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:  
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13: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB pep.\*  
14: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	352	97.5	67	9	US-09-852-424-1
3	352	97.5	67	9	US-09-852-424-9
4	348	96.4	67	9	US-09-852-424-7
5	347	96.1	67	9	US-09-852-424-3
6	347	96.1	67	9	US-09-852-424-6
7	345	95.6	67	9	US-09-852-424-2
8	344	95.3	67	9	US-09-852-424-8
9	344	95.3	67	9	US-09-852-424-1
10	344	95.3	67	10	US-09-144-838-8
11	344	95.3	67	10	US-09-144-838-23
12	344	95.3	89	8	US-08-927-939-22
13	344	95.3	89	9	US-09-792-793A-32
14	344	95.3	89	10	US-09-953-692-4
15	344	95.3	89	10	US-09-953-717-4
16	344	95.3	89	10	US-08-927-939-56
17	344	95.3	93	9	US-08-835-107-2
18	344	95.3	93	9	US-09-835-107-3
19	344	95.3	93	9	US-09-792-793A-93

20	344	95.3	93	10	US-09-144-838-7	Sequence 7, Appl
21	344	95.3	93	10	US-09-919-497-95	Sequence 99, Appl
22	344	95.3	320	9	US-09-792-793A-77	Sequence 77, Appl
23	344	95.3	322	9	US-09-792-793A-78	Sequence 78, Appl
24	344	95.3	327	9	US-09-792-793A-79	Sequence 79, Appl
25	342	94.7	67	9	US-09-852-424-4	Sequence 4, Appl
26	335.5	92.9	66	9	US-09-852-424-12	Sequence 12, Appl
27	333.5	92.4	66	9	US-09-852-424-10	Sequence 10, Appl
28	330.5	91.6	66	9	US-09-852-424-11	Sequence 11, Appl
29	327	90.6	68	10	US-09-144-838-51	Sequence 51, Appl
30	326.5	90.4	66	10	US-09-144-838-27	Sequence 27, Appl
31	309.5	85.7	67	10	US-09-144-838-47	Sequence 47, Appl
32	293	81.2	68	10	US-09-144-838-74	Sequence 24, Appl
33	290	80.3	67	10	US-09-144-838-25	Sequence 25, Appl
34	276	76.5	69	10	US-09-144-838-52	Sequence 52, Appl
35	275.5	76.3	67	10	US-09-144-838-28	Sequence 28, Appl
36	273	75.6	68	10	US-09-144-838-53	Sequence 53, Appl
37	258.5	71.6	68	10	US-09-144-838-48	Sequence 48, Appl
38	255.5	70.8	67	10	US-09-144-838-49	Sequence 49, Appl
39	252.5	69.9	66	10	US-09-144-838-29	Sequence 29, Appl
40	239	66.2	68	10	US-09-144-838-26	Sequence 26, Appl
41	222	61.5	69	10	US-09-144-838-54	Sequence 54, Appl
42	221.5	61.4	67	10	US-09-144-838-30	Sequence 30, Appl
43	221	61.2	67	10	US-09-144-838-31	Sequence 31, Appl
44	210.5	58.3	66	10	US-09-144-838-35	Sequence 35, Appl
45	204.5	56.6	68	10	US-09-144-838-50	Sequence 50, Appl

## ALIGNMENTS

RESULT 1  
US-09-852-424-5  
Sequence 5, Application US/09852424  
Patent No. US20020156034A1  
GENERAL INFORMATION:  
APPLICANT: The University of British Columbia; and  
APPLICANT: Chemokine Therapeutics Corporation  
TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: 80021-257  
CURRENT APPLICATION NUMBER: US/09/852,424  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: CA 2,305,787  
PRIOR FILING DATE: 2000-05-09  
PRIOR APPLICATION NUMBER: US 60/205,467  
NUMBER OF SEQ ID NOS: 135  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Engineered in  
US-09-852-424-5  
Query Match  
Best Local Similarity 100.0%; Score 361; Length 67;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 KGVSLSTPCPCRFESHVARAVKHLKILNTPCALQIYARLKNRRVCIDPKLWIDE 60  
QY 61 YLEKALN 67  
DB 61 YLEKALN 67  
RESULT 2  
US-09-852-424-1  
Sequence 1, Application US/09852424

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; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 67
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; US-09-852-424-1
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Query Match          97.5%; Score 352; DB 9; Length 67;
Best Local Similarity 98.5%; Pred. No. 9.7e-33;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 61 YLEKALN 67
DB 61 YLEKALN 67
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RESULT 3
US-09-852-424-9
; Sequence 9, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
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; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (8)
; OTHER INFORMATION: Xaa=P*-proline-amino acid chimera. See page 17 of
; OTHER INFORMATION: disclosure for possible structures for P*
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
; US-09-852-424-9
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Query Match          97.5%; Score 352; DB 9; Length 67;
Best Local Similarity 98.5%; Pred. No. 9.7e-33;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 61 YLEKALN 67
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US-09-852-424-7
; Sequence 7, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 67
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (6)
; OTHER INFORMATION: Xaa=P*-proline-amino acid chimera. See page 17 of
; OTHER INFORMATION: disclosure for possible structures for P*
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
; US-09-852-424-7
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Best Local Similarity 97.0%; Pred. No. 2.7e-32;
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OY 61 YLEKALN 67
DB 61 YLEKALN 67
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RESULT 5
US-09-852-424-3
; Sequence 3, Application US/09852424
; Patent No. US20020156034A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia; and
; APPLICANT: Chemokine Therapeutics Corporation
; TITLE OF INVENTION: CXCR4 ANTAGONIST TREATMENT OF HEMATOPOIETIC CELLS
; FILE REFERENCE: 80021-257
; CURRENT APPLICATION NUMBER: US/09/852,424
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 67
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Engineered in
; OTHER INFORMATION: Laboratory
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APPLICANT: Merzouk, Ahmed  
APPLICANT: Arab, Lakhdar  
APPLICANT: Saxena, Geeta  
APPLICANT: Eaves, Connie J.  
APPLICANT: Castman, Johanne  
APPLICANT: Clark-Lewis  
APPLICANT: Salari, Hassan  
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS  
FILE REFERENCE: SMAR012  
CURRENT APPLICATION NUMBER: US/09/835,107  
CURRENT FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: CA 2,305,036  
PRIOR FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: US 60/232,425  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: CA 2,335,109  
PRIOR FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: SDF-1 alpha  
US-09-835-107-1

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Best Local Similarity 97.0%; Pred. No. 7.5e-32;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 KPVSLSTRCPCFESHVARANYKHILNTPNCALQIYARLNNNNROYCIDPKLWIOE 60  
QY 61 YLEKALN 67  
DB 61 YLEKALN 67

RESULT 10  
US-09-144-838-8  
Sequence 8, Application US/09144838A  
Patent No. US20020051996A1  
GENERAL INFORMATION:  
APPLICANT: Siani, Michael A.  
APPLICANT: Wilken, Jill  
APPLICANT: Simon, Reyna  
APPLICANT: Kent, Stephen B.H.  
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation  
FILE REFERENCE: GRN-020/01US  
CURRENT APPLICATION NUMBER: US/09/144,838A  
CURRENT FILING DATE: 1998-08-31  
EARLIER APPLICATION NUMBER: US 60/057,620  
EARLIER FILING DATE: 1997-09-04  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-144-838-8

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Best Local Similarity 97.0%; Pred. No. 7.5e-32;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 YLEKALN 67  
DB 61 YLEKALN 67

RESULT 11  
US-09-144-838-23  
Sequence 23, Application US/09144838A  
Patent No. US20020051996A1  
GENERAL INFORMATION:  
APPLICANT: Siani, Michael A.  
APPLICANT: Wilken, Jill  
APPLICANT: Simon, Reyna  
APPLICANT: Kent, Stephen B.H.  
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation  
FILE REFERENCE: GRN-020/01US  
CURRENT APPLICATION NUMBER: US/09/144,838A  
CURRENT FILING DATE: 1998-08-31  
EARLIER APPLICATION NUMBER: US 60/057,620  
EARLIER FILING DATE: 1997-09-04  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 23  
LENGTH: 67  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-144-838-23

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Best Local Similarity 97.0%; Pred. No. 7.5e-32;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 KPVSLSTRCPCFESHVARANYKHILNTPNCALQIYARLNNNNROYCIDPKLWIOE 60  
QY 61 YLEKALN 67  
DB 61 YLEKALN 67

RESULT 12  
US-08-927-939-22  
Sequence 22, Application US/08927939  
Patent No. US20010006640A1  
GENERAL INFORMATION:  
APPLICANT: Grainger, David J.  
APPLICANT: Tatalick, Lauren Marie  
TITLE OF INVENTION: Compounds and methods to inhibit or  
TITLE OF INVENTION: augment an inflammatory response.  
FILE REFERENCE: 295.022US1  
CURRENT APPLICATION NUMBER: US/08/927,939  
CURRENT FILING DATE: 1997-09-11  
NUMBER OF SEQ ID NOS: 83  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 22  
LENGTH: 89  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-927-939-22

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Best Local Similarity 97.0%; Pred. No. 9.9e-32;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 YLEKALN 67



Db 82 YLEKALN 88

RESULT 13

US-09-792-793A-32  
; Sequence 32, Application US/09792793A  
; Patent No. US20020168370A1

GENERAL INFORMATION:

APPLICANT: McDonald, John R.

APPLICANT: Coggins, Philip

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
FILE REFERENCE: 25020-601D OTHER INFLAMMATORY CONDITIONS AND DISORDERS

CURRENT APPLICATION NUMBER: US/09/792,793A

NUMBER OF SEQ ID NOS: 93

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 32

LENGTH: 89

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: OTHER INFORMATION: Human Chemokine Polypeptide: Stromal cell-derived

OTHER INFORMATION: Factor-1-Alpha (SDF-1-Alpha)

PUBLICATION INFORMATION:

JOURNAL: Genomics

VOLUME: 28

PAGES: 495-500

DATE: 1995

US-09-792-793A-32

Query Match

Best Local Similarity 95.3%; Score 344; DB 9; Length 89;

Best Local Similarity 97.0%; Pred. No. 9.9e-32; Indels 0; Gaps 0;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 22 KVSLSYRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 81

QY 61 YLEKALN 67

DB 82 YLEKALN 88

RESULT 14

US-09-953-692-4

; Sequence 4, Application US/09953692

; Patent No. US20020107195A1

GENERAL INFORMATION:

APPLICANT: Shalley, Gupta K.

TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by

FILE REFERENCE: P50676C1 Administering Stromal Cell Derived Factor-1(

CURRENT APPLICATION NUMBER: US/09/953,692

PRIOR FILING DATE: 2001-09-17

PRIOR APPLICATION NUMBER: 09/358,624

PRIOR FILING DATE: 1999-07-21

PRIOR APPLICATION NUMBER: 60/093,596

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4

LENGTH: 89

TYPE: PRT

ORGANISM: Human

US-09-953-692-4

Query Match

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Best Local Similarity 97.0%; Pred. No. 9.9e-32; Indels 0; Gaps 0;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 82 YLEKALN 88

Db 22 KVSLSYRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 81

QY 61 YLEKALN 67

DB 82 YLEKALN 88

RESULT 15

US-09-953-717-4

; Sequence 4, Application US/09953717

; Patent No. US20020107196A1

GENERAL INFORMATION:

APPLICANT: Shalley, Gupta K.

TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by

FILE REFERENCE: P50676D1 Administering Stromal Cell Derived Factor-1(

CURRENT APPLICATION NUMBER: US/09/953,717

PRIOR FILING DATE: 2001-09-17

PRIOR APPLICATION NUMBER: 09/358,624

PRIOR FILING DATE: 1999-07-21

PRIOR APPLICATION NUMBER: 60/093,596

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4

LENGTH: 89

TYPE: PRT

ORGANISM: Human

US-09-953-717-4

Query Match

Best Local Similarity 95.3%; Score 344; DB 10; Length 89;

Best Local Similarity 97.0%; Pred. No. 9.9e-32; Indels 0; Gaps 0;

Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KGVSLSTPCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 60

DB 22 KVSLSYRCPCRFESHVARANVKHLKILNTPNCALQIVARLKNNNROYCIDPKLKWIOE 81

QY 61 YLEKALN 67

DB 82 YLEKALN 88

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Job time : 7.2 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2003, 15:31:02 : Search time 11.6 Seconds  
(without alignments)  
555.259 Million cell updates/sec

Title: US-09-852-424-5

Perfect score: 361

Sequence: 1 KGVSLSYPCPCRFESHVAR.....QVCIDPKLKNIGVLEKALN 67

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Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR\_73:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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6	93.5	25.9	91	1	A46539
7	91	25.2	95	2	JN0841
8	91	25.2	120	2	I48147
9	90.5	25.1	99	2	A37034
10	88.5	24.5	91	1	A28815
11	87	24.1	101	2	S42496
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19	81	22.4	120	2	JEO177
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29	73.5	20.4	96	2	JC3478

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31	73.5	20.4	100	2	I55614	macrophage inflamm
32	73.5	20.4	103	2	A26736	transformation-ind
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34	73.5	20.4	132	2	A57325	C-X-C chemokine Li
35	72.5	20.1	101	2	B28414	growth-regulated p
36	72.5	20.1	107	2	A28414	melanoma growth-st
37	72.5	20.1	114	2	A55010	neutrophil-activat
38	72.5	20.1	117	2	B44253	alveolar macrophag
39	72	19.9	92	2	A32393	macrophage inflamm
40	70.5	19.5	53	2	I64831	gene KC protein -
41	69.5	19.3	622	2	A45255	Dp71 protein - hum
42	69.5	19.3	3678	2	S28916	dystrophin - mouse
43	69.5	19.3	3685	1	A27605	dystrophin, muscle
44	69	19.1	93	2	B35673	platelet factor 4
45	68.5	19.0	104	1	PH04A	platelet factor 4

#### ALIGNMENTS

##### RESULT 1

G01540

Cytokine SDF-1-beta - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 26-Aug-1999

C:Accession: G01540

R:Spotila, L.D.

A:Reference number: G07697

A:Accession: G01540

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-93 <SPO>

A:Cross-references: EMBL:U16752; NID:q1272194; PID:9571508

C:Superfamily: beta-thromboglobulin

Query Match 95.3%; Score 344; DB 2; Length 93;  
Best Local Similarity 97.0%; Pred. No. 11e-34;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	KGVSLSYPCPCRFESHVARAVKHLKILTPNCALQIVARLNNNNROVCIDPKIKWIOE 60	
DB	22	KPVSLSYPCPCRFESHVARAVKHLKILTPNCALQIVARLNNNNROVCIDPKIKWIOE 81	
QY	61	YLEKALN 67	
DB	82	YLEKALN 88	
RESULT 2			
A53497			
pre-B-cell growth-stimulating factor precursor - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 20-Jun-2000			
C:Accession: A53497; I59582			
R:Nagasawa, T.; Kikutani, H.; Kishimoto, T.			
Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994			
A:Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.			
A:Reference number: A53497; MUID:94181581; PMID:8134392			
A:Accession: A53497			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-89 <NAG>			
A:Cross-references: GB:D21072; NID:q413905; PID:BA04648.1; PID:9468457			
A:Title: Signal sequence, tryp: a cloning strategy for secreted proteins and type I me			
A:Reference number: I59582; MUID:93342488; PMID:8342023			
A:Accession: I59582			
A:Status: preliminary; translated from GB/EMBL/DBDJ			
A:Molecule type: mRNA			
A:Residues: 1-89 <RES>			

A:Cross-references: GB:LI2029; NID:g393179; PIDN:AAA40100.1; PID:g393180  
 C:Genetics:  
 A:Gene: SDF-1-alpha  
 C:Superfamily: beta-thromboglobulin  
 C:Keywords: cytokine

Query Match 95.0%; Score 343; DB 2; Length 89;  
 Best Local Similarity 95.5%; Pred. No. 1.4e-34;  
 Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLSTPCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 DB 22 KPVSLSTPCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81  
 OY 61 YLEKALN 67  
 DB 82 YLEKALN 88

#### RESULT 3

I33416  
 Interleukin-8 homolog - mouse

C:Species: Mus sp. (mouse)  
 C:Date: 02-Aug-1996 #sequence-revision 02-Aug-1996 #text-change 05-Nov-1999  
 C:Accession: I33416  
 R:Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.  
 Exp. Cell Res. 215, 284-293, 1994  
 A:Title: Molecular cloning of TPRL, a gene whose expression is repressed by the tumor F  
 A:Reference number: I33416; MUID:95073497; PMID:7982471

A:Accession: I33416  
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-89 <RES>

A:Cross-references: GB:S74318; NID:g786393; PIDN:AA832650.1; PID:g786394

C:Genetics:

A:Gene: TPRL

C:Superfamily: beta-thromboglobulin

Query Match 95.0%; Score 343; DB 2; Length 89;  
 Best Local Similarity 95.5%; Pred. No. 1.4e-34;  
 Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLSTPCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 DB 22 KPVSLSTPCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81  
 OY 61 YLEKALN 67  
 DB 82 YLEKALN 88

#### RESULT 4

I81182  
 Cytokine - mouse

C:Species: Mus musculus (house mouse)  
 C:Date: 02-Aug-1996 #sequence-revision 02-Aug-1996 #text-change 05-Nov-1999  
 C:Accession: I81182  
 R:Tashiro, K.; Tada, H.; Heiker, R.; Shirozu, M.; Nakano, T.; Honjo, T.  
 Science 261, 600-603, 1993  
 A:Title: Signal sequence trap: a cloning strategy for secreted proteins and type I membr  
 A:Reference number: I59582; MUID:93342488; PMID:8342023

A:Accession: I81182

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-93 <RES>

A:Cross-references: GB:LI2030; NID:g393181; PIDN:AAA40101.1; PID:g393182

C:Genetics:

A:Gene: SDF-1-beta

C:Superfamily: beta-thromboglobulin

Query Match 95.0%; Score 343; DB 2; Length 93;  
 Best Local Similarity 95.5%; Pred. No. 1.4e-34;  
 Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLSTPCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60  
 DB 22 KPVSLSTPCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81

OY 61 YLEKALN 67  
 DB 82 YLEKALN 88

#### RESULT 5

I48148  
 Neutrophil attractant protein-1 - guinea pig

C:Species: Cavia porcellus (guinea pig)  
 C:Date: 02-Jul-1996 #sequence-revision 02-Jul-1996 #text-change 20-Aug-1999  
 C:Accession: I48148  
 R:Toshimura, T.; Johnson, D.G.  
 J. Immunol. 151, 6225-6236, 1993  
 A:Title: cDNA cloning and expression of guinea pig neutrophil attractant protein-1 (N  
 A:Reference number: I48148; MUID:94065176; PMID:7504015

A:Accession: I48148

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-101 <RES>

A:Cross-references: GB:LI04986; NID:g459764; PIDN:AAA37049.1; PID:g459765

C:Genetics:

A:Gene: NAP-1

C:Superfamily: beta-thromboglobulin

Query Match 27.1%; Score 98; DB 2; Length 101;  
 Best Local Similarity 34.4%; Pred. No. 9.9e-05;  
 Matches 21; Conservative 17; Mismatches 17; Indels 6; Gaps 4;

OY 11 CRFEESHVARAN--VKHLKILNTPNCA-LOIVARLKNNNRQVCIDPKLKWIOE 65  
 DB 34 CQCICKIHTTTPHFKFKELKVESGPCANSEITIVKL-SDNRQLCDPKKRWQDVVSMF 92

OY 66 L 66  
 DB 93 L 93

#### RESULT 6

A46539  
 monocyte chemoattractant cytokine RANTES precursor - mouse

N:Alternate names: Muranates

C:Species: Mus musculus (house mouse)

C:Date: 18-Jun-1993 #sequence-revision 16-Aug-1996 #text-change 22-Jun-1999

C:Accession: I48875; A46539; I48654; I56970

R:Danoff, T.M.; Lailley, P.A.; Chang, Y.S.; Heeger, P.S.; Neilson, E.G.

J. Immunol. 152, 1182-1189, 1994

A:Title: Cloning, genomic organization, and chromosomal localization of the Scya5 gen

A:Reference number: I48875; MUID:94132613; PMID:7507961

A:Accession: I48875

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-91 <DAN>

A:Cross-references: EMBL:U02298; NID:g460090; PIDN:AAA13302.1; PID:g460091

R:Schell, T.J.; Simpson, N.J.; Mak, J.Y.

Eur. J. Immunol. 22, 1477-1481, 1992

A:Title: Molecular cloning and expression of the murine RANTES cytokine: structural a

A:Reference number: A46539; MUID:92289805; PMID:1376260

A:Accession: A46539

A:Molecule type: mRNA

A:Residues: 1-18, 'A', '20-91 <SCH>

A:Cross-references: GB:S37648; NID:g250207; PIDN:AA822330.1; PID:g250208

A:Experimental source: macrophage cell line P05-1.8

A:Note: sequence extracted from NCBI backbone (NCBIN:106768, NCBIP:106770)

R:Shin, H.S.; Drysdale, B.E.; Shin, M.L.; Noble, P.W.; Fisher, S.N.; Paznekas, W.A.

Mol. Cell. Biol. 14, 2914-2925, 1994

A:Title: Definition of a lipopolysaccharide-responsive element in the 5'-flanking reg

A:Reference number: I48654; MUID:94217689; PMID:7513046

A:Accession: I48654

A:Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-91 <SH1>  
 A:Cross-references: EMBL:X70675; NID:g475205; PIDN:CAA50011.1; PID:g475206  
 R:McLison, E.G.; Krensky, A.  
 Kidney Int. 41, 220-225, 1992  
 A:Title: Isolation and characterization of cDNA from renal tubular epithelium encoding p  
 A:Reference number: 156970; MUID:92277990; PMID:1375672  
 A:Accession: 156970  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-40, 'E', 42-91 <NE1>  
 A:Cross-references: GB:M77747; NID:g200649; PIDN:AAA40029.1; PID:g200650  
 C:Comment: This chemottractant for monocytes but not neutrophils is an immediate-early  
 C:Genetics:  
 A:Introns: 26/71: 63/2  
 C:Superfamily: macrophage inflammatory protein  
 C:Keywords: chemokaxis; cytokine; immediate-early protein; inflammation  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-91/Product: monocyte chemottractant cytokine RANTES #status predicted <MAT>  
 Query Match 25.9%; Score 93.5; DB 1; Length 91;  
 Best Local Similarity 34.5%; Pred. No. 0.00031;  
 Matches 19; Conservative 10; Mismatches 25; Indels 1; Gaps 1;  
 Oy 8 PCPCFFESHVARAVNHKLILNTPNCALQIVARLKNNNROYCIDPKLWIOEYL 62  
 Db 32 PCCFAYLSLALPRAHVKY-FTTSSKCSMLAVFVTRNRKVCANPEKMWQVEYI 85  
 RESULT 7  
 JN0841  
 Interleukin-8 - dog  
 C:Species: Canis lupus familiaris (dog)  
 C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 12-Apr-1995  
 C:Accession: JN0841  
 R:Ishikawa, J.; Suzuki, S.; Hotta, K.; Hirota, Y.; Mizuno, S.; Suzuki, K.  
 Gene 131, 305-306, 1993  
 A:Title: Cloning of a canine gene homologous to the human Interleukin-8-encoding gene.  
 A:Reference number: JN0841; MUID:94010328; PMID:7916715  
 A:Accession: JN0841  
 A:Molecule type: DNA  
 A:Residues: 1-95 <ISH>  
 C:Comment: This protein is a polymorphonuclear leukocytes chemotactic factor and is invc  
 A:Introns: 22/71: 67/2  
 C:Superfamily: beta-thromboglobulin  
 Query Match 25.2%; Score 91; DB 2; Length 95;  
 Best Local Similarity 33.3%; Pred. No. 0.00066;  
 Matches 22; Conservative 15; Mismatches 21; Indels 8; Gaps 4;  
 Oy 3 VSLSPCCRFESHVARAVNHKLILNT---PNCA-LQIVARLKNNNROYCIDPKLW 57  
 Db 28 VSELRCOC-IKTHSTFPHPKYIKELRYDGPCHENSEIIVKLFNGN-EVCLDPKEKW 84  
 Oy 58 IOEYLE 63  
 Db 85 VQKVVO 90  
 RESULT 8  
 I48147  
 monocyte chemottractant protein-1 - guinea pig  
 C:Species: Cavia porcellus (guinea pig)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
 C:Accession: I48147  
 R:Yoshimura, T.  
 J. Immunol. 150, 5025-5032, 1993  
 A:Title: cDNA cloning of guinea pig monocyte chemottractant protein-1 and expression of  
 A:Reference number: I48147; MUID:93267104; PMID:8496603  
 A:Accession: I48147  
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
 A:Residues: 1-120 <RES>  
 A:Cross-references: GB:I04985; NID:g349820; PIDN:AAA37047.1; PID:g349821  
 C:Genetics:  
 A:Gene: MCP-1  
 C:Superfamily: macrophage inflammatory protein  
 Query Match 25.2%; Score 91; DB 2; Length 120;  
 Best Local Similarity 29.8%; Pred. No. 0.00085;  
 Matches 17; Conservative 10; Mismatches 30; Indels 0; Gaps 0;  
 Oy 8 PCPCFFESHVARAVNHKLILNTPNCALQIVARLKNNNROYCIDPKLWIOEYLEK 64  
 Db 31 PCCTCFENQIOLKRVKXGERTSSRCPEAVIFRLTKKEVCADPTQKMWQDIYAK 87  
 RESULT 9  
 A37034  
 Interleukin-8 precursor - human  
 N:Alternate names: beta-thromboglobulin-like protein; fibroblast-derived neutrophil-a  
 te-derived neutrophil chemotactic factor; monocyte-derived neutrophil-activating fact  
 C:Species: Homo sapiens (man)  
 C:Date: 08-Dec-1992 #sequence\_revision 08-Dec-1992 #text\_change 20-Aug-1999  
 C:Accession: A37034; JI0041; A37791; S37634; PLO107; A28598; A27488; A39960; A60401;  
 R:Mukaida, N.; Shiroo, M.; Matsushima, K.  
 J. Immunol. 143, 1366-1371, 1989  
 A:Title: Genomic structure of the human monocyte-derived neutrophil chemotactic facto  
 A:Reference number: A37034; MUID:89309826; PMID:265993  
 A:Accession: A37034  
 A:Molecule type: DNA  
 A:Residues: 1-99 <MKU>  
 A:Cross-references: GB:M28130; NID:g186367; PIDN:AAA59158.1; PID:g186368  
 A>Note: the authors failed to translate the last thirty-six nucleotides of the second  
 R:Matsushima, K.; Morishita, K.; Yoshimura, T.; Lavu, S.; Kobayashi, Y.; Lew, W.; App  
 J. Exp. Med. 167, 1883-1893, 1988  
 A:Title: Molecular cloning of a human monocyte-derived neutrophil chemotactic factor  
 A:Reference number: JI0041; MUID:88258376; PMID:3260265  
 A:Accession: JI0041  
 A:Molecule type: mRNA  
 A:Residues: 1-99 <MAL>  
 A:Cross-references: EMBL:Y00787; NID:g34518; PIDN:CAA68742.1; PID:g34519  
 A>Note: the sequence shows similarity to several platelet-derived factors, a v-src-in  
 R:Kowalski, J.; Denhardt, D.T.  
 Mol. Cell. Biol. 9, 1946-1957, 1989  
 A:Title: Regulation of the mRNA for monocyte-derived neutrophil-activating peptide in  
 A:Reference number: A3791; MUID:89313739; PMID:2664463  
 A:Accession: A3791  
 A:Molecule type: mRNA  
 A:Residues: 1-99 <KOW>  
 A:Cross-references: GB:M26383; NID:g188627; PIDN:AAA36323.1; PID:g188628  
 R:King, C.H.; Gordon, G.S.; Konieczkowski, M.; Sedot, J.R.  
 submitted to the EMBL Data Library, February 1992  
 A:Reference number: S37634  
 A:Accession: S37634  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-97 <KIN>  
 A:Cross-references: EMBL:Z11686; NID:g33958; PIDN:CAA77745.1; PID:g33959  
 R:Suzuki, K.; Miyasaka, H.; Ota, H.; Yamakawa, Y.; Tagawa, M.; Kuramoto, A.; Mizuno,  
 J. Exp. Med. 169, 1895-1901, 1989  
 A:Title: Purification and partial primary sequence of a chemotactic protein for polym  
 A:Reference number: PLO107; MUID:8927941; PMID:2659722  
 A:Accession: PLO107  
 A:Molecule type: Protein  
 A:Residues: 23-32, 'XR', 35, 'X', 37-52, 'L', 54 <SUZ>  
 A:Experimental source: lung giant cell carcinoma L065C  
 R:Gregory, H.; Young, J.; Schroeder, J.M.; Mrowietz, U.; Christophers, E.  
 Biochem. Biophys. Res. Commun. 151, 883-890, 1988  
 A:Title: Structure determination of a human lymphocyte derived neutrophil activating  
 A:Reference number: A28598; MUID:88162914; PMID:3279957  
 A:Accession: A28598  
 A:Molecule type: protein  
 A:Residues: 28-99 <GRD>

R.Waltz, A.; Peveril, P.; Aschauer, H.; Baggiolini, M.  
Biochem. Biophys. Res. Commun. 149, 755-761, 1987  
A>Title: Purification and amino acid sequencing of NAF, a novel neutrophil-activating factor  
A:Reference number: A27488; MUID:86106502; PMID:332281  
A:Accession: A27488  
A:Molecule type: protein  
A:Residues: 28-59 <MAL>  
R.Yoshimura, T.; Matsushima, K.; Tanabe, S.; Robinson, E.A.; Appella, E.; Oppenheim, J.J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 9233-9237, 1987  
A>Title: Purification of a human monocyte-derived neutrophil chemotactic factor that has  
A:Reference number: A39960; MUID:86097462; PMID:3480540  
A:Accession: A39960  
A:Molecule type: protein  
A:Residues: 28-69 <YOS>  
R.Schroeder, J.M.; Sticherling, M.; Henneicke, H.H.; Preissner, W.C.; Christophers, E.  
J. Immunol. 144, 2223-2233, 1990  
A>Title: IL-1alpha or tumor necrosis factor-alpha stimulate release of three NAP-1/IL-8  
A:Reference number: A60401; MUID:90187866; PMID:2179408  
A:Accession: A60401  
A:Molecule type: protein  
A:Residues: 23-32 <SCH>  
A:Experimental source: dermal fibroblasts  
A>Note: a minor component of this material (15%) includes an additional two amino acids  
R.Van Damme, J.; Decock, B.; Conings, R.; Lenaerts, J.P.; Opdenacker, G.; Billiau, A.  
Eur. J. Immunol. 19, 1189-1194, 1989  
A>Title: The chemotactic activity for granulocytes produced by virally infected fibroblasts  
A:Reference number: A60591; MUID:89338542; PMID:2668011  
A:Accession: A60591  
A:Molecule type: protein  
A:Residues: 23-33, 'X', '35', 'X', '37-42 <VAN>  
R.Nakagawa, H.; Hatakeyama, S.; Ikeue, A.; Miyai, H.  
FEBS Lett. 282, 412-414, 1991  
A>Title: Generation of Interleukin-8 by plasmin from AVLPR-interleukin-8, the human fibroblast  
A:Reference number: S15827; MUID:91243843; PMID:1828038  
A:Accession: S15827  
A:Molecule type: protein  
A:Residues: 23-33, 'X', '35', 'X', '37-47 <FEH>  
R.van Damme, J.; Van Beeumen, J.; Conings, R.; Decock, B.; Billiau, A.  
Eur. J. Biochem. 181, 337-344, 1989  
A>Title: Purification of granulocyte chemotactic peptide/interleukin-8 reveals N-terminal  
A:Reference number: S04216; MUID:89231715; PMID:2523801  
A:Accession: S04216  
A:Molecule type: protein  
A:Residues: 21-67 <VA2>  
R.Yoshimura, T.; Robinson, E.A.; Appella, E.; Matsushima, K.; Showalter, S.D.; Skeel, A.  
Mol. Immunol. 26, 87-93, 1989  
A>Title: Three forms of monocyte-derived neutrophil chemotactic factor (MDNCF) distinguish  
A:Reference number: A60567; MUID:89181632; PMID:2648135  
A:Accession: A60567  
A:Molecule type: protein  
A:Residues: 21-33, 'X', '35', 'X', '37-47 <Y02>  
A>Note: the forms starting from positions 21, 23, and 28 represented 8%, 47%, and 45%,  
R.Van Damme, J.; Van Beeumen, J.; Opdenacker, G.; Billiau, A.  
J. Exp. Med. 167, 1364-1376, 1988  
A>Title: A novel, NH-2-terminal sequence-characterized human monokine possessing neutrophil  
A:Reference number: A60847; MUID:88187604; PMID:3258625  
A:Accession: A60847  
A:Molecule type: protein  
A:Residues: 28-47 <VA3>  
R.Car, B.D.; Baggiolini, M.; Waltz, A.  
Biochem. J. 275, 581-584, 1991  
A>Title: Formation of neutrophil-activating peptide 2 from platelet-derived connective-tissue  
A:Reference number: S15417; MUID:91248085; PMID:2039437  
A:Accession: S15417  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 28-99 <CAR>  
R.Golds, E.E.; Mason, P.; Myrjos, P.  
Biochem. J. 259, 585-588, 1989  
A>Title: Inflammatory cytokines induce synthesis and secretion of gro protein and a neutrophil  
A:Reference number: S03975; MUID:89246368; PMID:2655583  
A:Accession: S03975  
A:Molecule type: protein

A:Residues: 23-46 <GOL>  
R:Hotta, K.; Hayashi, K.; Ishikawa, J.; Tagawa, M.; Hashimoto, K.; Mizuno, S.; Suzuki  
Immunol. Lett. 24, 165-170, 1990  
A:Title: Coding region structure of interleukin-8 gene of human lung giant cell carcinoma  
A:Reference number: 154560; MUID:90346419; PMID:12200751  
A:Accession: 154560  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-99 <RES>  
A:Cross-references: GB:D14283; NID:g219915; PIDN:BA03245.1; PID:g219916  
R:Schmid, J.; Weissmann, C.  
J. Immunol. 139, 250-256, 1987  
A:Title: Induction of mRNA for a serine protease and a beta-thromboglobulin-like protein  
A:Reference number: 155992; MUID:87224164; PMID:2953813  
A:Accession: 155992  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-99 <RE2>  
A:Cross-references: GB:M17017; NID:g179579; PIDN:AAA3611.1; PID:g179580  
R:Kusner, D.J.; Luebers, E.L.; Nowinski, R.J.; Konieczkowski, M.; Kling, C.H.; Sedor,  
Kidney Int. 39, 1240-1248, 1991  
A:Title: Cytokine- and IPS-induced synthesis of interleukin-8 from human mesangial cells  
A:Reference number: 137902; MUID:91374977; PMID:1895676  
A:Accession: 137902  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-97 <RE3>  
A:Cross-references: EMBL:Z11686; NID:g33958; PIDN:CAA77745.1; PID:g33959  
R:Alouani, S.; Gaertner, H.F.; Mettoud, J.J.; Power, C.A.; Bacon, K.B.; Wells, T.N.C.;  
Eur. J. Biochem. 227, 328-334, 1995  
A:Title: A fluorescent interleukin-8 receptor probe produced by targeted labelling a  
A:Reference number: S67519; MUID:95154308; PMID:7851404  
A:Accession: S67519  
A:Molecule type: mRNA  
A:Residues: 1-99 <ALO>  
C:Comment: This secretory protein is chemotactic for polymorphonuclear leukocytes.  
C:Comment: This protein is variably processed at the amino end. The major form differ  
C:Genetics:  
A:Gene: GDB:IL8  
A:Cross-references: GDB:120099; OMIM:146930  
A:Map position: 4q13-4q21  
A:Introns: 22/1; 67/2; 95/2  
C:Superfamily: beta-thromboglobulin  
C:Keywords: chemotaxis; cytokine; inflammation  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-99/Product: interleukin-8, minor form #status experimental <MAT>  
F:23-99/Product: interleukin-8, major fibroblast-derived form #status experimental <M  
F:28-99/Product: interleukin-8, major lymphocyte/monocyte-derived form #status experi

Query	Best Match	Query Similarity	Score	DB	Length
23 VKHLKILNT-PNCA-IQTIVARKNNRQVCDPKLKIQLQYLEKAL 66	49 IKELRVIESGPHCAETETIVKL-SDGRELCIDPKENWQVRVEKFL 93	17; Conservative	25.1%; 37.0%; 16; Mismatches 10; Indels 3; Gaps 3;	25.1%; 37.0%; 16; Mismatches 10; Indels 3; Gaps 3;	25.1%; 37.0%; 16; Mismatches 10; Indels 3; Gaps 3;

RESULT 10  
A28815  
monocyte chemoattractant cytokine RANTES precursor - human  
N:Alternate names: small inducible cytokine A5; T-cell specific cytokine RANTES  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1989 #sequence\_revision 16-Aug-1996 #text\_change 29-May-1998  
C:Accession: A28815  
R:Schall, T.J.; Jongstra, J.; Dyer, B.J.; Jorgensen, J.; Clayberger, C.; Davis, M.M.;  
J. Immunol. 141, 1018-1025, 1988  
A:Title: A human T cell-specific molecule is a member of a new gene family.  
A:Reference number: A28815; MUID:88285659; PMID:2456327  
A:Accession: A28815  
A:Molecule type: mRNA  
A:Residues: 1-91 <SCH>  
A:Cross-references: GB:M21121

C:Comment: The acronym RANTES reflects the description "Regulated upon Activation, Normal C:Genetics:  
A:Gene: GDB:SCYA5: D17S136E  
A:Cross-references: GDB:120749; OMIM:187011  
A:Map position: 1/q11.2-17q12  
C:Superfamily: macrophage inflammatory protein  
C:Keywords: chemotaxis; cytokine; immediate-early protein; inflammation; T-cell  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-91/Product: T-cell protein RANTES #status predicted <MAT>

Query Match 24.5%; Score 88.5; DB 1; Length 91;  
Best Local Similarity 30.9%; Pred. No. 0.0033;  
Matches 17; Conservative 12; Mismatches 25; Indels 1; Gaps 1;

OY 8 PCPCRFESHVARANKHLKILNTPNCA-LQIYARLKNNNROYCIDPKLWIOEYL 62  
DB 32 PCCEFAIARLPRAHRIKEY-FYTSKSCSNPAAVFAVRKRNKOVCANPEKRWREYI 85

RESULT 11  
SA2496  
Interleukin-8 precursor [similarity] - sheep  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 19-Jan-2001  
C:Accession: S42496; 146997  
R:Legestols, I.; Greenland, T.; Arnaud, P.; Mornex, J.F.; Cordier, G.  
submitted to the EMBL Data Library, March 1994  
A:Description: Nucleotide sequence of ovine Interleukin 8 cDNA using polymerase chain re  
A:Reference number: S42496  
A:Accession: S42496  
A:Molecule type: mRNA  
A:Residues: 1-101 <LEG>  
A:Cross-references: EMBL:X78306; NID:9463253; PIDN:CAA55115.1; PID:9463254  
R:Seow, H.F.; Yoshimura, T.; Wood, P.R.; Colditz, I.G.  
Immunol. Cell Biol. 72, 398-405, 1994  
A:Title: Cloning, sequencing, expression and inflammatory activity in skin of ovine Inte  
A:Reference number: 146997; MUID:95137691; PMID:835984  
A:Accession: 146997  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-101 <SEO>  
A:Cross-references: GB:S74436; NID:9786590; PIDN:AA833241.1; PID:9786591  
C:Genetics:  
A:Gene: IL-8  
C:Superfamily: beta-thromboglobulin  
C:Keywords: chemotaxis; cytokine; inflammation  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-101/Product: Interleukin-8 #status predicted <MAT>

Query Match 24.1%; Score 87; DB 2; Length 101;  
Best Local Similarity 29.5%; Pred. No. 0.0022;  
Matches 18; Conservative 20; Mismatches 17; Indels 6; Gaps 4;

OY 11 CFFPESHVARAN---VKHLKILNT-PNCA-LQIYARLKNNNROYCIDPKLWIOEYLEKA 65  
DB 34 CCCTHTSPHPKFIKELRVIESGPHCENSEIIVKL-TNGKEVCLDPKKNVQKVF 92

OY 66 L 66  
DB 93 L 93

RESULT 12  
A32954  
gro-alpha precursor - mouse  
N:Alternate names: gro protein; growth regulated protein; melanoma growth-stimulating ac  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Oct-1989 #sequence\_revision 20-Oct-1999 #text\_change 20-Aug-1999  
C:Accession: A32954; JH0081  
R:Quendo, P.; Alberta, J.; Wen, D.; Graycar, J.L.; Derynck, R.; Stiles, C.D.  
J. Biol. Chem. 264, 4133-4137, 1989  
A:Title: The platelet-derived growth factor-inducible KC gene encodes a secretory protei  
A:Reference number: A32954; MUID:89139485; PMID:2917992

A:Accession: A32954  
A:Molecule type: mRNA  
A:Residues: 1-96 <QOU>  
A:Cross-references: GB:J04596; NID:9201042; PIDN:AAA40131.1; PID:9201043  
R:Ryseck, R.P.; MacDonald-Bravo, H.; Matzel, M.G.; Bravo, R.  
Exp. Cell Res. 180, 266-275, 1989  
A:Title: Cloning and sequence of a secretory protein induced by growth factors in mou  
A:Reference number: JH0081; MUID:89078502; PMID:2909392  
A:Accession: JH0081  
A:Molecule type: mRNA  
A:Residues: 1-96 <RYS>  
C:Comment: This protein is basic and lacks threonine, phenylalanine, and tyrosine.  
C:Genetics:  
A:Map position: 5  
C:Superfamily: beta-thromboglobulin  
C:Keywords: extracellular protein  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-96/Product: gro-alpha #status predicted <MAT>

Query Match 24.0%; Score 86.5; DB 2; Length 96;  
Best Local Similarity 31.7%; Pred. No. 0.0024;  
Matches 19; Conservative 17; Mismatches 21; Indels 3; Gaps 3;

OY 9 CPCRFEHVAVRANKHLKIL-NTNCA-LQIYARLKNNNROYCIDPKLWIOEYLEKA 66  
DB 33 CCCLQTMAGIKHLKNIQSLKVLPSGPHCTQTEVATLK-NGREACLDPEAPLVQKIVQKML 91

RESULT 13  
A53096  
Interleukin-8 precursor - pig  
N:Alternate names: alveolar macrophage chemotactic factor-1 (AMCF-1)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 02-Jun-1995 #sequence\_revision 02-Jun-1995 #text\_change 19-Jan-2001  
C:Accession: A53096; A44253  
R:Lin, G.; Pearson, A.E.; Scamurra, R.W.; Zhou, Y.; Baarsch, M.J.; Weiss, D.J.; Murta  
J. Biol. Chem. 269, 77-85, 1994  
A:Title: Regulation of interleukin-8 expression in porcine alveolar macrophages by ba  
A:Reference number: A53096; MUID:94103307; PMID:8276881  
A:Accession: A53096  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-103 <LIN>  
A:Cross-references: GB:M69923; NID:9164520; PIDN:AAA16616.1; PID:9164521  
R:Goodman, R.B.; Foster, D.C.; Mathewes, S.L.; Osborn, S.G.; Kulper, J.L.; Forstrom,  
Biochemistry 31, 10483-10490, 1992  
A:Title: Molecular cloning of porcine alveolar macrophage-derived neutrophil chemotac  
A:Reference number: A44253; MUID:93041741; PMID:1420165  
A:Accession: A44253  
A:Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 1-22, 'D', 24-103 <GOO>  
A:Cross-references: GB:M9367; NID:91235611  
A:Experimental source: alveolar macrophage  
A:Note: sequence extracted from NCBI backbone (NCBIN:117415, NCBI:117416)  
C:Superfamily: beta-thromboglobulin  
C:Keywords: chemotaxis; cytokine; inflammation  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-103/Product: Interleukin-8 #status predicted <MAT>

Query Match 23.5%; Score 85; DB 2; Length 103;  
Best Local Similarity 30.3%; Pred. No. 0.0039;  
Matches 20; Conservative 18; Mismatches 20; Indels 8; Gaps 5;

OY 3 VSLSPCPCRFESHVARAN---VKHLKILNT-PNCA-LQIYARLKNNNROYCIDPKLW 57  
DB 28 VSAELRCQC--INTHTSPHPKFIKELRVIESGPHCENSEIIVKL-TNGKEVCLDPKKN 84

OY 58 IOEYLE 63  
DB 85 VQKVVQ 90

## RESULT 14

A54678

monocyte chemotactic protein 3 precursor - human

N:Alternate names: monocyte chemoattractant protein MCP-3

C:Species: Homo sapiens (man)

C:Date: 28-Oct-1994 #sequence, revision 28-Oct-1994 #text\_change 16-Jul-1999

C:Accession: A54678; JCI478; S32222

R:Opdenakker, G.; Flieten, P.; Nys, G.; Froyen, G.; Van Roy, N.; Speleman, F.; Laureys, G.

Genomics 21, 403-408, 1994

A:Title: The human MCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the

A:Reference number: A54678; MUID:94375065; PMID:7916328

A:Accession: A54678

A:Molecule type: DNA

A:Residues: 1-109 &lt;OPD&gt;

R:Opdenakker, G.; Froyen, G.; Flieten, P.; Proost, P.; Van Damme, J.

Biochem. Biophys. Res. Commun. 191, 535-542, 1993

A:Title: Human monocyte chemotactic protein-3 (MCP-3): Molecular cloning of the cDNA and

A:Reference number: JCI478; MUID:93213290; PMID:8461011

A:Accession: JCI478

A:Molecule type: mRNA

A:Residues: 1-109 &lt;OP2&gt;

A:Cross-References: GB:X72308; GB:S57464; NID:93928270; PIDN:CAA51055.1; PID:9313708

R:Miny, A.; Chalon, P.; Guillemet, J.C.; Kagnad, M.; Lauzun, P.; Magazin, M.; Miloux,

submitted to the EMBL Data Library, March 1993

A:Description: Molecular cloning of MCP-3: a human monocyte-derived monocyte chemoatrac

A:Reference number: S32222

A:Accession: S32222

A:Molecule type: mRNA

A:Residues: 1-109 &lt;MIN&gt;

A:Cross-References: EMBL:X71087; NID:9288396; PIDN:CAA50405.1; PID:9288397

C:Comment: This protein induces proteinase secretion and chemotaxis by macrophages and m

C:Genetics:

A:Gene: GDB:SCYA7; SCYA6; MCP-3

A:Cross-References: GDB:138473; OMIM:158106

A:Map position: 17q11-17q12

A:Introns: 36/1; 75/2

A:Superfamily: macrophage inflammatory protein

C:Keywords: cytokine; glycoprotein; inflammation

F:1-33/Domain: signal sequence #status predicted &lt;SIG&gt;

F:34-109/Product: monocyte chemotactic protein 3 #status predicted &lt;MAT&gt;

F:39/Binding site: carboxylate (Asn) (covalent) #status predicted

## Query Match

Best Local Similarity 23.5%; Score 85; DB 2; Length 109;

Matches 13; Conservative 19; Mismatches 30; Indels 0; Gaps 0;

QY 2 GVSLSYPCPCRFESHVARANVHKLILNTPNCALQIVARLKNNRQVCIDPKLKIQEX 61

DB 37 GINTSTTCYRFTNKKIPKORLESYRRTSSHCPRAVIFKTKLDREICADPTQKWVDF 96

QY 62 LE 63

DB 97 MK 98

## RESULT 15

A41130

dystrophin homolog - Pacific electric ray (fragment)

N:Alternate names: 300k subynaptic protein

C:Species: Torpedo californica (Pacific electric ray)

C:Date: 03-Aug-1992 #sequence, revision 03-Aug-1992 #text\_change 16-Jul-1999

C:Accession: A41130

R:Yeadon, J.E.; Lin, H.; Dyer, S.M.; Burden, S.J.

J. Cell Biol. 115, 1069-1076, 1991

A:Title: Dystrophin is a component of the subynaptic membrane.

A:Reference number: A41130; MUID:92064638; PMID:1720119

A:Accession: A41130

A:Molecule type: mRNA

A:Residues: 1-870 &lt;YEA&gt;

A:Cross-References: GB:M37645

C:Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystrop

F:2-129/Domain: spectrin/dystrophin repeat homology <SP1>  
F:131-238/Domain: spectrin/dystrophin repeat homology <SP2>  
F:253-290/Domain: WW repeat homology <WW1>

## Query Match

Best Local Similarity 23.4%; Score 84.5; DB 2; Length 870;

Matches 20; Conservative 7; Mismatches 27; Indels 5; Gaps 1;

QY 5 LSYPCPCRFESHVARANVHKLILNTPNCALQIVARLKN-----NRQVCIDPKLKI 58

DB 322 LSLPSCAEAFDQHNKQNDQLDILEITNCTSIYDRLEQEHNNVNPICVDMCLNWL 380

Search completed: January 23, 2003, 15:37:25  
Job time : 11.6 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 23, 2003, 15:28:07 : Search time 6 Seconds

(without alignments)  
463.152 Million cell updates/sec

Title: US-09-852-424-5

Sequence: 1 KGVSLSYPCPCRFESHVAR.....QVCIDPKLKIQVEYLERALN 67

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	344	95.3	93	1	SDF1_FELCA
2	344	95.3	93	1	SDF1_HUMAN
3	343	95.0	89	1	SDF1_MOUSE
4	98	27.1	101	1	IL8_CAVPO
5	94	26.0	101	1	IL8_CANFA
6	93.5	25.9	91	1	SY05_MOUSE
7	93.5	25.9	92	1	SY05_RAT
8	91	25.2	101	1	IL8_FELCA
9	91	25.2	120	1	SY02_CAVPO
10	90.5	25.1	99	1	IL8_HUMAN
11	88.5	24.5	91	1	SY05_HUMAN
12	87.5	24.2	91	1	SY05_CAVPO
13	87.5	24.1	101	1	IL8_MCMU
14	87	24.2	101	1	IL8_SHEEP
15	86.5	24.0	96	1	GRO_MOUSE
16	85.5	23.7	101	1	IL8_CERTO
17	85	23.5	99	1	SY07_HUMAN
18	85	23.5	103	1	IL8_PIG
19	84.5	23.4	98	1	SY13_HUMAN
20	84	23.3	101	1	IL8_BOVIN
21	84	23.3	101	1	IL8_RABIT
22	83.5	23.1	91	1	SY05_BOVIN
23	83	23.0	97	1	SY08_MOUSE
24	83	23.0	130	1	SY05_RAT
25	82.5	22.9	96	1	GRO_RAT
26	82	22.7	50	1	SY05_PIG
27	81.5	22.6	92	1	SY03_RAT
28	81	22.4	148	1	SY02_MOUSE
29	81	22.4	148	1	SY02_RAT
30	80	22.2	120	1	SY16_HUMAN
31	79	21.9	89	1	SY18_HUMAN
32	78.5	21.7	100	1	MP2_MOUSE
33	78	21.6	119	1	SY24_MOUSE

34	77.5	21.5	97	1	EDTA_MOUSE
35	77.5	21.5	114	1	SZ06_HUMAN
36	76.5	21.2	71	1	GRO1_RABIT
37	76.5	21.2	112	1	SZ06_BOVIN
38	76.5	21.2	119	1	SZ07_PIG
39	76	21.1	96	1	EDTA_CAVPO
40	75.5	20.9	97	1	EDTA_RAT
41	75.5	20.9	107	1	MI2B_HUMAN
42	73.5	20.4	92	1	SY04_RABIT
43	73.5	20.4	100	1	MP2_RAT
44	73.5	20.4	103	1	EMF1_CHICK
45	73.5	20.4	132	1	SZ05_MOUSE

## ALIGNMENTS

### RESULT 1

ID SDF1\_FELCA STANDARD: PRT: 93 AA.

AC 062657;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12).  
GN SDF1.

OS Fells silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.

RC TISSUE=Thymus;  
RA MEDLINE=98450506; PubMed=9777331;  
RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K.,  
RA Cai J.S., Sato E., Kohmoto M., Mikami T.;  
RT "Molecular cloning and sequencing of feline stromal cell-derived factor-1 alpha and beta";  
RL Eur. J. Immunogenet. 25:303-305(1998).

CC -1- FUNCTION: CHEMOKINE-INDUCED ACTIVATION OF T-LYMPHOCYTES, MONOCYTES, BUT NOT NEUTROPHILS.  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXC).

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CC EMBL: AB011966; BAA28602.1; -  
CC HSSP: P48061; ISDE.  
DR InterPro: IPR001089; CXC\_chim\_kine\_sm1.  
DR InterPro: IPR001811; Chemokine\_IL8.  
DR Pfam: PF00048; IL8; 1.  
DR SMART: SM00199; SCY; 1.  
DR PROSITE: PS00471; SMALL\_CYTOKINES\_CXC; FALSE\_NEG.  
KW Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing.  
FT SIGNAL 1 19  
FT CHAIN 20 93  
FT DISULFID 30 55  
FT FT 32 71  
FT VARSPIC 90 93  
FT SEQUENCE 93 AA; 10581 MW; 44FC763711E9BE37 CRC64;

Query Match 95.38; Score 344; DB 1; Length 93;  
Best local Similarity 97.0%; Pred. No. 2e-35;  
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY      1 KGVSLSYPCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
DB      22 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81
QY      61 YLEKALN 67
DB      82 YLEKALN 88

RESULT 2
SDFL_HUMAN STANDARD; PRT; 93 AA.
ID      SDFL_HUMAN
AC      P48061;
DT      01-FEB-1996 (Rel. 33, Created)
DT      01-FEB-1996 (Rel. 33, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell
GN      growth stimulating factor) (PBSF) (HHRH).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Spottila L.D.;
RL      Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=96039262; PubMed=7490086;
RA      Shirizu M., Nakano T., Inazawa J., Tashiro K., Tada H.,
RA      Shinohara T., Honjo T.;
RT      "Structure and chromosomal localization of the human stromal cell-
RT      derived factor 1 (SDF1) gene.";
RL      Genomics 28:495-500(1995).
RN      [3]
RP      SEQUENCE FROM N.A. (ISOFORM ALPHA).
RA      Tissue-Liver;
RC      begun N.A., Barnard G.F.;
RT      "Nucleotide sequence of hHRH, human intercrine reduced in
RT      hepatomas.";
RL      Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      STRUCTURE BY NMR OF 22-88.
RA      MEDLINE=98046030; PubMed=9384579;
RA      Crump M.P., Gong J.H., Loetscher P., Rajaratnam K., Amara A.,
RA      Arenzana-Seisdedos F., Virelizier J.L., Baggiolini M., Sykes B.D.,
RA      Clark-Lewis I.;
RT      "Solution structure and basis for functional activity of stromal
RT      cell-derived factor-1, dissociation of CXCR4 activation from binding
RT      and inhibition of HIV-1.";
RL      EMBO J. 16:6996-7007(1997).
RN      [5]
RP      X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-88.
RA      MEDLINE=98284037; PubMed=9618518;
RA      Dealwis C., Fernandez E.J., Thompson D.A., Simon R.J., Siani M.A.,
RA      Lolis E.;
RT      "Crystal structure of chemically synthesized [N3A] stromal
RT      cell-derived factor 1alpha, a potent ligand for the HIV-1 'fusin'
RT      coreceptor.";
RL      Proc. Natl. Acad. Sci. U.S.A. 95:6941-6946(1998).
RN      [6]
RP      FUNCTION: CHEMOTACTANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT
RN      NOT NEUTROPHILS.
RN      [7]
RP      ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE);
RN      ARE PRODUCED BY ALTERNATIVE SPLICING.
RN      [8]
RP      SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
RN      C-X-C) (CHEMOKINE CXC).
RN      [9]
RP      This SWISS-PROT entry is copyright. It is produced through a collaboration
RN      between the Swiss Institute of Bioinformatics and the EMBL outstation -
RN      the European Bioinformatics Institute. There are no restrictions on its
RN      use by non-profit institutions as long as its content is in no way
RN      modified and this statement is not removed. Usage by and for commercial

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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: U16752; AA97434.1; -
DR      EMBL: L36033; AAB39332.1; -
DR      EMBL: L36034; AAB39333.1; -
DR      EMBL: U19495; AAB40516.1; -
DR      PDB: 1SDF; 28-JAN-98.
DR      PDB: 2SDF; 17-JUN-98.
DR      PDB: 1A15; 12-AUG-98.
DR      Genew; HGNC:10672; SDF1.
DR      MTM; 600835; -
DR      Interpro; IPR001089; CXC_chemkine_sm1.
DR      Interpro; IPR001811; Chemokine_IL8.
DR      Pfam; PF00048; IL8; 1.
DR      SMART; SM00199; SCY; 1.
DR      PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
KW      Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing;
KW      3D-structure.
FT      SIGNAL 1 19 POTENTIAL.
FT      CHAIN 20 93 STROMAL CELL-DERIVED FACTOR 1.
FT      DISULFID 30 55
FT      DISULFID 32 71
FT      VARSPIC 90 93 MISSING (IN ISOFORM ALPHA).
SQ      SEQUENCE 93 AA; 10666 MW; 505B5A29C2B44EBD CRC64;

Query Match 95.3%; Score 344; DB 1; Length 93;
Best Local Similarity 97.0%; Pred. No. 2e-35;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 KGVSLSYPCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 60
DB      22 KPVSLSYRCPCRFESHVARANKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIOE 81
QY      61 YLEKALN 67
DB      82 YLEKALN 88

RESULT 3
SDFL_MOUSE STANDARD; PRT; 89 AA.
ID      SDFL_MOUSE
AC      P40224;
DT      01-FEB-1995 (Rel. 31, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell
DE      growth stimulating factor) (PBSF) (12-O-tetradecanoylphorbol 13-
DE      acetate repressed protein 1) (TPAR1) (Thymic lymphoma cell stimulating
DE      factor) (TISF).
GN      SDFL.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=94181581; PubMed=8134392;
RA      Nagasawa T., Kikutani H., Kishimoto T.;
RT      "Molecular cloning and structure of a pre-B-cell growth-stimulating
RT      factor.";
RL      Proc. Natl. Acad. Sci. U.S.A. 91:2305-2309(1994).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=93342488; PubMed=8342023;
RA      Tashiro K., Tada H., Heliker R., Shirizu M., Nakano T., Honjo T.;
RT      "Signal sequence trap: a cloning strategy for secreted proteins and
RT      type I membrane proteins.";
RL      Science 261:600-603(1993).
RN      [3]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=95073497; PubMed=7982471;
RA      Jiang W., Zhou P., Kahn S.M., Tomita N., Johnson M.D.,

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RA Weinstein I.B.:
RT "Molecular cloning of TPAP1, a gene whose expression is repressed by
RT the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA).";
RL Exp. Cell Res. 215:284-293(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=AKR/J;
RA Nomura M., Nakata Y., Nose M., Akashi M., Suzuki G.;
RL Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CHEMOTACTICANT ACTIVE ON T-LYMPHOCYTES, MONOCYTES, BUT
CC NOT NEUTROPHILS.
CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF BONE MARROW-DERIVED B
CC PRECURSOR CELLS IN THE PRESENCE OF IL-7 AS WELL AS GROWTH OF THE
CC STROMAL CELL-DEPENDENT B-CELL CLONE DM34 CELLS.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE);
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE INTERCINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
CC -----
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CC -----
DR EMBL: D21072; BAA04648.1; -
DR EMBL: L12029; AAA40100.1; -
DR EMBL: L12030; AAA40101.1; -
DR EMBL: S74318; AAB32650.1; -
DR EMBL: D43804; BAA07862.1; -
DR EMBL: D43805; BAA07863.1; -
DR PIR: A53497; A53497.
DR HSSP: P48061; 1SDP.
DR MGD: MGI:103556; Sdfl.
DR InterPro: IPR001089; CXC_cmkine_sm11.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
DR KMW: Cytokine; Chemotaxis; Growth factor; Signal; Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 89 STROMAL CELL-DERIVED FACTOR 1.
FT DISULFID 30 55 BY SIMILARITY.
FT DISULFID 32 71 BY SIMILARITY.
FT VARSPLIC 89 89 K -> KRLKM (IN ISOFORM BETA).
SQ SEQUENCE 89 AA; 10032 MW; C4B8AD69078E55FA CRC64;

Query Match
Best Local Similarity 95.0%; Score 343; DB 1; Length 89;
Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLSTYPCRFREFSHVARANKHLINTPCALQIVARLKNNNROYCIDPKLWIOE 60
DB 22 KPVSLSTYPCRFREFSHVARANKHLINTPCALQIVARLKNNNROYCIDPKLWIOE 81
OY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 4
IL8_CANVO STANDARD: PRT: 101 AA.
AC P49113;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8) (Neutrophil attractant protein
DE 1) (NAP-1).
GN IL8.
OS Cavia porcellus (Guinea pig).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathia; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=94065176; PubMed=7504015;
RA Yoshimura T., Johnson D.G.;
RT "cdna cloning and expression of guinea pig neutrophil attractant
RT protein-1 (NAP-1). NAP-1 is highly conserved in guinea pig.";
RL J. Immunol. 151:6225-6236(1993).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERCINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
CC -----
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CC -----
DR EMBL: L04986; AAA37049.1; -
DR HSSP: P10145; 21L8.
DR InterPro: IPR001089; CXC_cmkine_sm11.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTKCXC.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
DR KMW: Cytokine; Chemotaxis; Inflammatory response; Signal.
FT SIGNAL 1 22
FT CHAIN 23 101 INTERLEUKIN-8.
FT DISULFID 34 61 BY SIMILARITY.
FT DISULFID 36 77 BY SIMILARITY.
SQ SEQUENCE 101 AA; 11414 MW; 557E2A9E15F6727F CRC64;

Query Match
Best Local Similarity 27.1%; Score 98; DB 1; Length 101;
Matches 21; Conservative 17; Mismatches 17; Indels 6; Gaps 4;

OY 11 CRFESHVARAN--VKHLKIINT-PCNA-LQIVARLKNNNROYCIDPKLWIOEYLEKA 65
DB 34 CQCIKHTTPEHPKPKFKELKVIESGPCANSEIIVL-SDNRQLCDLPKKWQDVVSMF 92
OY 66 L 66
DB 93 L 93

RESULT 5
IL8_CANFA STANDARD: PRT: 101 AA.
AC P41324;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN IL8.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94010328; PubMed=7916715;
RA Ishikawa J., Suzuki S., Hotta K., Hirota Y., Mizuno S., Suzuki K.;
RT "Cloning of a canine gene homologous to the human

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RT Interleukin-8-encoding gene."
RL Gene 131:305-306(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Lymph node;
RX MEDLINE=95127913; PubMed=7827282;
RA Matsumoto Y., Mohamed A., Onodera T., Kato H., Ohashi T.,
RA Goltzuka R., Tsujimoto H., Hasegawa A., Furusawa S., Yoshinara K.,
RA Ishikawa J., Hotta K., Suzuki K., Hirota Y.;
RT "Molecular cloning and expression of canine Interleukin 8 cDNA."
RL Cytokine 6:455-461(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-Mongrel; TISSUE-Jugular vein;
RX MEDLINE=95114148; PubMed=7814650;
RA Kukiela G.L., Smith W.C., Larosa G.J., Manning A.M.,
RA Mendoza L.H., Daly T.J., Hughes B.J., Youker K.A., Hawkins H.K.,
RA Michael L.H., Rot A., Entman M.L.;
RT "Interleukin-8 gene induction in the myocardium after ischemia and
RT reperfusion in vivo."
RL J. Clin. Invest. 95:89-103(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Beagle;
RX MEDLINE=97230298; PubMed=9119462;
RA Straubinger R.K., Straubinger A.F., Harter L., Jacobson R.H.,
RA Chang Y.-F., Summers B.A., Erb H.N., Appel M.J.;
RT "Borrelia burgdorferi migrates into joint capsules and causes an up-
RT regulation of interleukin-8 in synovial membranes of dogs
RL infect. Immun. 65:1273-1285(1997).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CX-C).
CC -----
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CC -----
DR EMBL: D28772; BAA05961.1; -
DR EMBL: D14285; BAA03246.1; -
DR EMBL: U10308; AAC48434.1; -
DR EMBL: AF048717; AAC05134.1; -
DR HSSP: P10145; 1IKM
DR InterPro: IPR001089; CX-C_chemkine_smll
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTCKCX.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Chemotaxis; Inflammatory response; Signal.
FT SIGNAL 1 22
FT CHAIN 23 101 BY SIMILARITY.
FT DISULFID 34 61 INTERLEUKIN-8.
FT DISULFID 36 77 BY SIMILARITY.
SQ SEQUENCE 101 AA; 11280 MW; 3A3A4676DA968376 CRC64;
Query Match 26.0%; Score 94; DB 1; Length 101;
Best Local Similarity 34.7%; Pred. No. 9,6e-05;
Matches 25; Conservative 15; Mismatches 20; Indels 12; Gaps 5;
QY 3 VSLSYPCPCFPFESHVAVKAKVHLKILNT-----PNCV-LDITVARKNNNOVCIDPKLKW 57
DB 28 VSSELRCQC--IKTHSPFHPKPKYIKELRLVIDSGPHENSELIVKLVNGN--EVCIDPKPKW 84

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QY 58 IQE----YLEKA 65
DB 85 VQKVQVFFLKKA 96
RESULT 6
SY05_MOUSE STANDARD; PRT; 91 AA.
ID SY05_MOUSE
AC P30882;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small-inducible cytokine A5 precursor (CC15) (T-cell specific RANTES
DE protein) (Sis-delta) (Murantes).
GN SCYAS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92277990; PubMed=1375672;
RA Heeger P., Wolf G., Meyers C., Sun M.J., O'Farrell S.C.,
RA Krensky A.M., Neilson E.G.;
RT "Isolation and characterization of cDNA from renal tubular epithelium
RT encoding murine Rantes."
RL Kidney Int. 41:220-225(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92289805; PubMed=1376260;
RA Schall T.J., Simpson N.J., Mak J.Y.;
RT "Molecular cloning and expression of the murine RANTES cytokine;
RT structural and functional conservation between mouse and man."
RL Eur. J. Immunol. 22:1477-1481(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NIH Swiss;
RX MEDLINE=94132613; PubMed=7507961;
RA Danoff T.M., Lalley P.A., Chang Y.S., Heeger P.S., Neilson E.G.;
RT "Cloning, genomic organization and chromosomal localization of the
RT Scy5 gene encoding the murine chemokine RANTES."
RL J. Immunol. 152:1182-1189(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=94217689; PubMed=7513046;
RA Shih H.S., Drysdale B.E., Shih M.L., Noble P.W., Fisher S.N.,
RA Paznekas W.A.;
RT "Definition of a lipopolysaccharide-responsive element in the 5'-
RT flanking regions of Murantes and crg-2."
RL Mol. Cell. Biol. 14:2914-2925(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/CJ.B10.S/J, NOD/LTJ, and SJL/J; TISSUE=Spleen;
RA Ma R.Z., Teuscher C.;
RT Submitted (May-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
CC BASOPHILS AND ACTIVATES EOSINOPHILS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: T-CELL AND MACROPHAGE SPECIFIC.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
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CC -----
EMBL: M77747; AAA40029.1; -

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DR EMBL: S37648; AAB2330.1; -  
DR EMBL: U02298; AAA18302.1; -  
DR EMBL: X70675; CAA5001.1; -  
DR EMBL: AF065944; AAC17511.1; -  
DR EMBL: AF065945; AAC17512.1; -  
DR EMBL: AF065946; AAC17513.1; -  
DR EMBL: AF065947; AAC17514.1; -  
DR HSP: P13501; IRTN.  
DR MGD: MG1:98262; Scya5.  
DR InterPro: IPR000827; CC-chemkine_sm1.  
DR InterPro: IPR001811; Chemokine_il8.  
DR Pfam: PF00048; Il8; 1.  
DR SMART: SM00199; SCY; 1.  
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.  
KW cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.  
FT SIGNAL 1 23  
FT CHAIN 1 91  
FT DISULFID 34 57  
FT DISULFID 33 73  
FT CONFLICT 19 19  
FT CONFLICT 41 41  
SQ SEQUENCE 91 AA: 10071 MW: 5DPD66F4684FE1C8 CRC64;  
  
Query March 25.9%; Score 93.5; DB 1: Length 91:  
Best Local Similarity 34.5%; Pred. No. 9.9e-05;  
Matches 19: Conservative 10; Mismatches 25; Indels 1; Gaps 1;  
  
QY 8 PCPCRFESHAVRANVKKHLKILNPNCALQIYARCKNNRRQCIDPKIKWIDEYL 62  
Db 32 PCCFAYLSLAPRAHVKEY-FYTSSKCSNLAVFYTRNRRCVCANPEKKWQEIY 85  
|||:::||||:|-|-|||:::||||:  
RESULT 7  
SY05_RAT STANDARD: PRT; 92 AA.  
AC PS0231:  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Small inducible cytokine A5 precursor (CCLS) ('T'-cell specific RANTES protein) (SIS-delta).  
GN SCYA5.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Long Evans; TISSUE=Lung;  
RA Jones W.L., Shanley T.P., Ward P.A.;  
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.  
CC -! FUNCTION: CHEMOTACTANT FOR BLOOD MONOCYTES. MEMORY T HELPER CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).  
CC -! SUBCELLULAR LOCATION: Secreted.  
CC -! SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMKINE CC).  
-----  
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CC -----  
DR EMBL: U06436; AAA9649.1; -  
DR HSP: P13501; IRTN.  
DR InterPro: IPR000827; CC-chemkine_sm1.  
DR InterPro: IPR001811; Chemokine_il8.  
DR Pfam: PF00048; Il8; 1.  
DR SMART: SM00199; SCY; 1.  
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
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KW Cytokine, Chemotaxis; T-cell; Signal; Inflammatory response.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 92 SMALL INDUCIBLE CYTOKINE A5.
FT DISULFID 34 58 BY SIMILARITY.
FT DISULFID 35 74 BY SIMILARITY.
SQ SEQUENCE 92 AA; 10170 MW; B4PDECBA4208ABC6 CRC64;

Query Match 25.9%; Score 93.5; DB 1; Length 92;
Best Local Similarity 34.5%; Pred. No. 0.0001;
Matches 19; Conservative 10; Mismatches 25; Indels 1; Gaps 1;

QY 8 PCPCFFSHVARNVKHLKILNTPNCALQIYARKLNRRNOVCIDPKIKMIOEYL 62
DB 33 PCCFAYLSLAPRAHVKEY-FYTSSKCSNLAVFYTRRNOVCANPEKKWOEYI 86

RESULT 8
IL8_FELCA
AC IL8_FELCA STANDARD; PRT; 101 AA.
ID Q9XSX5;
DR 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN IL8
OS Felis silvestris catus (Cat).
OC Euryarchaea; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
CC NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Straubinger A.F., Simpson K.W., Straubinger R.K.;
RL "Feline interleukin-8 mRNA."
RL Submitted (JUN-1999) to the EMBL/Genbank/DDBJ databases.
CC - FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
CC - SUBUNIT: HOMODIMER (BY SIMILARITY).
CC - SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXCL8).
CC -----
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CC -----
CC EMBL: AF158598; AAD40323.1; -
CC DR HSP: P10145; IIRK.
CC DR InterPro: IPRO01089; CXCL_chmkine.sm11.
CC DR InterPro: IPRO01811; Chemokine_IL8.
CC Pfam: PF00048; IL8; 1.
CC PRINTS: PR00437; SMALLCYTKXC.
CC SMART: SMO0199; SCY; 1.
CC PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
CC Cytokine; Chemotaxis; Inflammatory response; Signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 101 INTERLEUKIN-8.
FT DISULFID 34 61 BY SIMILARITY.
FT DISULFID 36 77 BY SIMILARITY.
SQ SEQUENCE 101 AA; 11165 MW; 690DD97F13EPF9170 CNC64;

Query Match 25.2%; Score 91; DB 1; Length 101;
Best Local Similarity 32.8%; Pred. No. 0.00022;
Matches 19; Conservative 18; Mismatches 15; Indels 6; Gaps 4;

QY 11 CRFFSHVARN---VKHLKILNT-PNCA-LQIVARKLNRRNOVCIDPKIKMIOEYLE 63
DB 34 CCCTFHSTPFPPKLIKELTVIDSPPHCNSNTITVKNL-NGEVYCLDPKRKMVRQAVE 90

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RESULT 9
ID SY02_CAVPO STANDARD: PRT: 120 AA.
AC 008782;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1)..
GN SCYA2 OR MCP1.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=; TISSUE=Spleen;
RX MEDLINE=93267104; PubMed=8496603;
RA Yoshimura T.;
RT "CDNA cloning of guinea pig monocyte chemoattractant protein-1 and
RT expression of the recombinant protein.";
RL J. Immunol. 150:5025-5032(1993).
CC -1- FUNCTION: CHEMOTACTIC FACTOR THAT ATTRACTS MONOCYTES, BUT NOT
CC NEUTROPHILS.
CC -1- SUBUNIT: MONOMER OR HOMODIMER; IN EQUILIBRIUM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
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DR EMBL: L04985; AAA37047.1; .
DR HSSP: P80098; 1B00.
DR InterPro: IPR000827; CC.Chemkine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
KW Cytokine; Chemotaxis; Signal; Inflammatory response; Glycoprotein.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 120 SMALL INDUCIBLE CYTOKINE A2.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT DISULFID 33 57 BY SIMILARITY.
FT DISULFID 34 73 BY SIMILARITY.
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 120 AA: 13741 MW: 5905596851CFIC54 CRC64;

Query Match 25.2%; Score 91; DB 1; Length 120;
Best Local Similarity 29.8%; Pred. No. 0.00027;
Matches 17; Conservative 10; Mismatches 30; Indels 0; Gaps 0;

OY 8 PCPCFFESHVAVANKHLKILNTPGALQIYARLKNNNROYCIDPKLKWIDEYLEK 64
DB 31 PRCYTFNKPQIPLKRKVGERTITSRCPQEAIVFRTLKNKEVCADPTQWVDYIAK 87

RESULT 10
ID IL8_HUMAN STANDARD: PRT: 99 AA.
AC P10145; Q9C077; Q96R66;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8) (Monocyte-derived neutrophil
DE chemotactic factor) (MDCNF) (T-cell chemotactic factor) (Neutrophil-

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DE activating protein 1) (NAP-1) (Lymphocyte-derived neutrophil-
DE activating factor) (LYNAP) (Protein 3-10C) (Neutrophil-activating
DE factor) (NAF) (Granulocyte chemotactic protein 1) (GCP-1) (Enoctakin).
GN IL8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88258376; PubMed=3260265;
RA Matsushima K., Morishita K., Yoshimura T., Lavu S., Kobayashi Y.,
RA Lew W., Appella E., Kung H., Leonard E.J., Oppenheim J.J.;
RT "Molecular cloning of a human monocyte-derived neutrophil chemotactic
RT factor (MDCNF) and the induction of MDCNF mRNA by interleukin 1 and
RT tumor necrosis factor."
RL J. Exp. Med. 167:1883-1893(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87224164; PubMed=2953813;
RA Schmid J., Weissmann C.;
RT "Induction of mRNA for a serine protease and a
RT beta-thromboglobulin-like protein in mitogen-stimulated human
RT leukocytes."
RL J. Immunol. 139:250-256(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89313739; PubMed=2664463;
RA Kowalski J., Denhardt D.T.;
RT "Regulation of the mRNA for monocyte-derived neutrophil-activating
RT peptide in differentiating HL60 promyelocytes."
RL Mol. Cell. Biol. 9:1946-1957(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=89309626; PubMed=2663993;
RA Mukaida N., Shitoo M., Matsushima K.;
RT "Genomic structure of the human monocyte-derived neutrophil
RT chemotactic factor IL-8."
RL J. Immunol. 143:1366-1371(1989).
RN [5]
RP SEQUENCE FROM N.A.
RA Ishikawa J.;
RT Submitted (JAN-1993) to the EMBL/Genbank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Jang J.S., Kim B.E.;
RT Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Yi Q.,
RA Nickerson D.A.;
RT Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
RN [8]
RP SEQUENCE OF 23-46.
RX MEDLINE=89246368; PubMed=2655583;
RA Golds E.E., Mason P., Nyirkos P.;
RT "Inflammatory cytokines induce synthesis and secretion of gro protein
RT and a neutrophil chemotactic factor but not beta 2-microglobulin in
RT human synovial cells and fibroblasts."
RL Biochem. J. 259:585-588(1989).
RN [9]
RP SEQUENCE OF 23-54.
RX MEDLINE=89279141; PubMed=2659722;
RA Suzuki K., Miyasaka H., Ota H., Yamakawa Y., Tagawa M., Kuramoto A.,
RA Mizuno S.;
RT "Purification and partial primary sequence of a chemotactic protein
RT for polymorphonuclear leukocytes derived from human lung giant cell
RT carcinoma LU65C cells."
RL J. Exp. Med. 169:1895-1901(1989).
RN [10]
RP SEQUENCE OF 28-99.
RX MEDLINE=88162914; PubMed=3279957;
RA Gregory H., Young J., Schroeder J.M., Mrowietz U., Christophers E.;

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RT "Structure determination of a human lymphocyte derived neutrophil  
RT activating peptide (LYMAP).";  
RL Biochem. Biophys. Res. Commun. 151:883-890(1988).  
RN [11]  
RP SEQUENCE OF 28-59.  
RX MEDLINE=88106502; PubMed=3322281;  
RA Walz A., Peverl P., Aschauer H., Baggiolini M.;  
RT "Purification and amino acid sequencing of NAF, a novel neutrophil-  
RL activating factor produced by monocytes.";  
RL Biochem. Biophys. Res. Commun. 149:755-761(1987).  
RN [12]  
RP SEQUENCE OF 28-69.  
RX MEDLINE=88097462; PubMed=3480540;  
RA Yoshimura T., Matsushima K., Tanaka S., Robinson E.A., Appella E.,  
RT Oppenheim J.J., Leonard E.J.;  
RT "Purification of a human monocyte-derived neutrophil chemotactic  
RT factor that has peptide sequence similarity to other host defense  
RT cytokines";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:9233-9237(1987).  
RN [13]  
RP N-TERMINAL FORMS.  
RX MEDLINE=91006326; PubMed=2145175;  
RA van Damme J., Rampart M., Coning R., Decock B., van Osselaer N.,  
RT Williams J., Billiau A.;  
RT "The neutrophil-activating proteins interleukin 8 and beta-  
RT thromboglobulin: In vitro and in vivo comparison of NH2-terminally  
RT processed forms.";  
RL Eur. J. Immunol. 20:2113-2118(1990).  
RN [14]  
RP N-TERMINAL FORMS.  
RX MEDLINE=89231715; PubMed=2532801;  
RA van Damme J., van Beeumen J., Conings R., Decock B., Billiau A.;  
RT "Purification of granulocyte chemotactic peptide/interleukin-8  
RT reveals N-terminal sequence heterogeneity similar to that of  
RT beta-thromboglobulin.";  
RL Eur. J. Biochem. 181:337-344(1989).  
RN [15]  
RP SYNTHESIS OF 28-99.  
RX MEDLINE=91175767; PubMed=2007144;  
RA Clark-Lewis I., Mose B., Walz A., Baggiolini M., Scott G.J.,  
RT Abersold R.;  
RL "Chemical synthesis, purification, and characterization of two  
RT inflammatory proteins, neutrophil activating peptide 1  
RT (interleukin-8) and neutrophil activating peptide.";  
RL Biochemistry 30:3128-3135(1991).  
RN [16]  
RP REVIEW.  
RX MEDLINE=92347562; PubMed=1639201;  
RA Baggiolini M., Clark-Lewis I.;  
RT "Interleukin-8, a chemotactic and inflammatory cytokine.";  
RL FEBS Lett. 307:97-101(1992).  
RN [17]  
RP STRUCTURE BY NMR.  
RX MEDLINE=90234679; PubMed=2184886;  
RA Clore G.M., Appella E., Yamada M., Matsushima K., Gronenborn A.M.;  
RT "Three-dimensional structure of interleukin 8 in solution.";  
RL Biochemistry 29:1689-1696(1990).  
RN [18]  
RP STRUCTURE BY NMR OF COMPLEX TO RECEPTOR.  
RX MEDLINE=99148123; PubMed=10368283;  
RA Skelton N.J., Quan C., Reilly D., Lowman H.;  
RT "Structure of a CXCR chemokine-receptor fragment in complex with  
RT interleukin-8";  
RL Structure 7:157-168(1999).  
RN [19]  
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
RX MEDLINE=90216714; PubMed=2182630;  
RA Baldwin E.T., Franklin K.A., Appella E., Yamada M., Matsushima K.,  
RT Wlodawer A., Weber I.T.;  
RT "Crystallization of human interleukin-8. A protein chemotactic for  
RT neutrophils and T-lymphocytes.";  
RL J. Biol. Chem. 265:6851-6853(1990).  
RN [20]

[illegible]

RX MEDLINE=88285659; PubMed=2456327;  
 RA Schall T.J., Jongstra J., Dyer B.J., Jorgensen J., Clayberger C.,  
 RA Davis M.M., Krensky A.M.;  
 RT "A human T cell-specific molecule is a member of a new gene family.";  
 RL J. Immunol. 141:1018-1025(1988).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RA Jang J.S., Kim B.E.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=99228475; PubMed=10213461;  
 RA Nomiyama H., Fukuda S., Ito M., Tanase S., Miura R., Yoshie O.;  
 RT "Organization of the chemokine gene cluster on human chromosome  
 RT 17q11.2 containing the genes for CC chemokine MIP-1, HCC-2, LEC, and  
 RT RANTES.";  
 RL J. Interferon Cytokine Res. 19:227-234(1999).  
 RN [4]  
 RN SEQUENCE FROM N.A.  
 RA Zeng Q.P., Yang R.Y., Fu L.C.;  
 RT "The complete sequence of human beta-chemokine RANTES mRNA.";  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RL Strausberg R.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RN SEQUENCE OF 49-56; 71-79 AND 83-91, AND FUNCTION.  
 RX MEDLINE=96106406; PubMed=8525373;  
 RA Cocchi F., Devico A.L., Garzino-Demo A., Arya S.K., Gallo R.C.,  
 RA Lusso P.;  
 RT "Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major  
 RT HIV-suppressive factors produced by CD8+ T cells.";  
 RL Science 270:1811-1815(1995).  
 RN [7]  
 RN STRUCTURE BY NMR.  
 RX MEDLINE=95352612; PubMed=7542919;  
 RA Chung C.-W., Cooke R.M., Proudfoot A.E.I., Wells T.N.C.;  
 RT "The three-dimensional solution structure of RANTES.";  
 RL Biochemistry 34:9307-9314(1995).  
 RN [8]  
 RN STRUCTURE BY NMR.  
 RX MEDLINE=95244456; PubMed=7537088;  
 RA Skelton N.J., Aspinas F., Ogez J., Schall T.J.;  
 RT "Proton NMR assignments and solution conformation of RANTES, a  
 RT chemokine of the C-C type.";  
 RL Biochemistry 34:5329-5342(1995).  
 RN [9]  
 RN SYNTHESIS, AND X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 RX MEDLINE=9911238; PubMed=9889151;  
 RA Wilken J., Hoover D., Thompson D.A., Barlow P.N., Mesparion H.,  
 RA Picard L., Mlodaver A., Lubkowski J., Kent S.B.;  
 RT "Total chemical synthesis and high-resolution crystal structure of  
 RT the potent anti-HIV protein AOP-RANTES.";  
 RL Chem. Biol. 6:43-51(1999).  
 RN [10]  
 RN X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 RA Hoover D.M., Shaw J., Gryczynski Z., Proudfoot A.E.I., Wells T.N.C.,  
 RA Lubkowski J.;  
 RT "The crystal structure of Met-RANTES: comparison with native RANTES  
 RT and AOP-RANTES.";  
 RL Protein Pept. Lett. 7:73-82(2000).  
 CC -1- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER  
 CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM  
 CC BASOPHILS AND ACTIVATES EOSINOPHILS. BINDS TO CCR1, CCR3, CCR4 AND  
 CC CCR5. ONE OF THE MAJOR HIV-SUPPRESSIVE FACTORS PRODUCED BY CD8+ T  
 CC CELLS. RECOMBINANT RANTES PROTEIN INDUCES A DOSE-DEPENDENT  
 CC INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2, AND SIMIAN  
 CC IMMUNODEFICIENCY VIRUS (SIV).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: T-CELL AND MACROPHAGE SPECIFIC.  
 CC -1- INDUCTION: BY MITOGENS.

CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE  
 CC C-C) (CHEMOKINE CC).  
 CC -----  
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 CC -----  
 DR EMBL: M21121; AAA36725.1; -  
 DR EMBL: AF043341; AAC03541.1; -  
 DR EMBL: AF088219; AAC63331.1; -  
 DR EMBL: AF266753; AAF73070.1; -  
 DR EMBL: BC008600; AAH08600.1; -  
 DR PIR: A28815; A28815  
 DR PDB: 1HRJ; 14-OCT-96.  
 DR PDB: 1RTN; 03-JUN-95.  
 DR PDB: 1RTO; 03-JUN-95.  
 DR PDB: 1B3A; 23-APR-99.  
 DR PDB: 1EQT; 19-APR-00.  
 DR Genew; HGNC:10632; SCYA5.  
 DR MIM; 187011; -  
 DR InterPro; IPR000827; CC\_chemkine\_sml.  
 DR InterPro; IPR001811; Chemokine\_IL8.  
 DR Pfam; PF00048; IL8; 1.  
 DR SMART; SM00199; SCY; 1.  
 DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
 DR Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response;  
 KW 3D-structure.  
 FT SIGNAL 1 23  
 FT CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5.  
 FT DISULFID 33 57  
 FT DISULFID 34 73  
 FT CONFLICT 7 7 A -> R (IN REF. 1 AND 4).  
 FT CONFLICT 14 14 A -> V (IN REF. 4).  
 SQ SEQUENCE 91 AA; 9990 MW; FB0BFAFA87C620F CRC64;  
 Query Match 24.5%; Score 88.5; DB 1; Length 91;  
 Best Local Similarity 30.9%; Pred. No. 0.00041;  
 Matches 17; Conservative 12; Mismatches 25; Indels 1; Gaps 1;  
 QY 8 PCPCRFESHVARANYKHLKILTPNCALQIVARLKNRNROVCIDPRKWIQYEL 62  
 DB 32 PCCFATVATRLPRAHIKEY-FYISGRCSNPAVVFVTRKNNOVCANDEKKWVREYI 85  
 ID SY05\_CAVPO STANDARD; PRT; 91 AA.  
 AC P97272; 009076;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES  
 DE protein) (SIS-delta).  
 GN SCYA5.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=Dunkin-Hartley;  
 RA Campbell E.M., Proudfoot A.E.I., Yoshimura T., Allet B.,  
 RA Wells T.N.C., White A.M., Westwick J., Watson M.L.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Asano K., Nakamura M., Oguma T., Fukunaga K., Ishizaka A.,  
 RA Yamaguchi K., Kanazawa M.;



```
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CHEMOTACTRANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CC CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
CC BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CC).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U77037; AAC53293.1; -.
CC EMBL: AB002662; BA019604.1; -.
CC HSSP: P13501; 1RTN.
CC InterPro: IPR000827; CC_chemkine_sml.
CC InterPro: IPR001811; Chemokine_IL8.
CC Pfam: PF00048; IL8; 1.
CC SMART: SM00199; SCY; 1.
CC PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
CC Cyclokin: Chemotaxis; T-cell; Signal; Inflammatory response.
CC SIGNAL 1 23
CC CHAIN 24 91 POTENTIAL.
CC FT DISULFID 33 57 BY SIMILARITY.
CC FT DISULFID 34 73 BY SIMILARITY.
CC SEQUENCE 91 AA: 10088 MW: 766A31B751237DB9 CRC64:
CC
Query Match 24.2%; Score 87.5; DB 1; Length 91;
Best Local Similarity 33.9%; Pred. No. 0.00054;
Matches 19; Conservative 14; Mismatches 18; Indels 5; Gaps 3;
Oy 10 PCRFESHVARANVK-HLK--ILNTPNCALQIVARLKNNNRQVCIDPKLKWIOEYL 62
Db 32 PCCF-AVISRALPRTHIKKEYFYTSSKSNLAVFVETKRNQVCANPEKKWREYI 85
RESULT 13
IL8_MACMU STANDARD: PRT: 101 AA.
AC P51495:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN IL8.
OS Macaca mulatta (Rhesus macaque), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; TISSUE=Blood;
RX MEDLINE=95355132; PubMed=7628861;
RA Minerly J.C., Baganoft M.P., Depeleer C.L., Keller B.T.,
RA Rapp S.R., Widomski D.L., Fretland D.J., Bolanowski M.A.;
RT "Identification and characterization of rhesus macaque
RT Interleukin-8.";
RL Inflammation 19:313-331(1995).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
```

```
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXCL).
CC -----
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CC -----
CC EMBL: U19849; AAA86711.1; -.
CC EMBL: U19851; AAA86713.1; -.
CC EMBL: S78555; AAA80141.2; -.
CC HSSP: P10145; 2IL8.
CC InterPro: IPR001089; CXCL_chemkine_sml.
CC InterPro: IPR001811; Chemokine_IL8.
CC Pfam: PF00048; IL8; 1.
CC SMART: PR00437; SMALLCYTOKXC.
CC PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
CC Cyclokin: Chemotaxis; Inflammatory response; Signal.
CC SIGNAL 1 22
CC CHAIN 23 101 BY SIMILARITY.
CC FT DISULFID 34 61 BY SIMILARITY.
CC FT DISULFID 36 77 BY SIMILARITY.
CC SEQUENCE 101 AA: 11320 MW: 42BCF9C97C84B5F9 CRC64:
CC
Query Match 24.2%; Score 87.5; DB 1; Length 101;
Best Local Similarity 36.4%; Pred. No. 0.0006;
Matches 16; Conservative 16; Mismatches 9; Indels 3; Gaps 3;
Oy 23 VKHLKIWT-PCNA-LQIVARLKNNNRQVCIDPKLKWIOEYLEK 64
Db 49 IKELRVIESGPCANTETIIVKL-SQGRELCIDPKPEWQRYVEK 91
RESULT 14
IL8_SHEEP STANDARD: PRT: 101 AA.
AC P36925:
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-8 precursor (IL-8) (CXCL8).
GN IL8.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95121931; PubMed=7821808;
RA Legasteleis I., Greenland T., Arnaud P., Mornex J.F., Cordier G.;
RT "Sequencing of the ovine Interleukin-8-encoding cDNA using the
RT polymerase chain reaction.";
RL Gene 150:367-369(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95137691; PubMed=7835984;
RA Seow H.F., Yoshimura T., Wood P.R., Colditz I.G.;
RT "Cloning, sequencing, expression and inflammatory activity in skin of
RT ovine interleukin-8.";
RL Immunol. Cell Biol. 72:398-405(1994).
CC -1- FUNCTION: IL-8 IS A CHEMOTACTIC FACTOR THAT ATTRACTS NEUTROPHILS,
CC BASOPHILS, AND T-CELLS, BUT NOT MONOCYTES. IT IS ALSO INVOLVED IN
CC NEUTROPHIL ACTIVATION. IT IS RELEASED FROM SEVERAL CELL TYPES IN
CC RESPONSE TO AN INFLAMMATORY STIMULUS.
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RESULT 2
Q90ZD1 PRELIMINARY: PRT: 89 AA.
AC Q90ZD1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Stromal cell-derived factor-1 alpha.
GN SDF-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Ohtani Y., Okada M., Kawaguchi N., Minami M., Satoh M.;
RT "CDNA cloning of rat stromal cell-derived factor-1 alpha (SDF-1
alpha).";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Pillarisetti K., Gupta S.K.;
RT "Identification and molecular cloning of a novel rat ortholog of the
RT alpha chemokine, stromal cell derived factor-1 (SDF-1).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF189724; AAF01066.1; -.
DR EMBL: AF209976; AAG43506.1; -.
DR HSP: P48061; ISDF.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
SQ SEQUENCE 89 AA; 9977 MW; D86977626A2E35FA CRC64;

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Query Match 93.1%; Score 336; DB 11; Length 89;
Best Local Similarity 94.0%; Pred. No. 1.4e-34;
Matches 63; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 KGVSLSPCCRFESHVARANKHLKILNTPNCALQIYARLKNRRQVCIDPKLKWIOE 60
DB 22 KPVSLSYRCPREFESHVARANKHLKILNTPNCALQIYARLKNRRQVCIDPKLKWIOE 81
OY 61 YLEKALN 67
DB 82 YLEKALN 88

RESULT 3
Q80UJ9 PRELIMINARY: PRT: 94 AA.
AC Q80UJ9;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Stromal-derived factor 1 precursor.
GN SDF-1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Braun M., Wunderlin M., Knoechel W., Gierschik P., Moepf B.;
RT "Xenopus laevis stromal-derived factor 1: conservation of structure
RT and function during vertebrate development.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ278857; CAC82196.1; -.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
KW Signal.

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FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 94 STROMAL-DERIVED FACTOR 1.
SQ SEQUENCE 94 AA; 10701 MW; 8C8325D152F326E7 CRC64;

Query Match 77.0%; Score 278; DB 13; Length 94;
Best Local Similarity 73.1%; Pred. No. 2.7e-27;
Matches 49; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

OY 1 KGVSLSPCCRFESHVARANKHLKILNTPNCALQIYARLKNRRQVCIDPKLKWIOE 60
DB 22 KPVSLSYRCPREFESHVARANKHLKILNTPNCALQIYARLKNRRQVCIDPKLKWIOE 81
OY 61 YLEKALN 67
DB 82 YLEKALN 88

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RESULT 4
Q91ZL1 PRELIMINARY: PRT: 91 AA.
AC Q91ZL1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE RANPES Chemokine.
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RA Blanco J.C., Pletneva L.M., Prince G.A.;
RT "Sigmodon hispidus cytokines, chemokines and interferons.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF421391; AAL16932.1; -.
DR InterPro: IPR000827; CC_Chemokine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; UNKNOWN.1.
SQ SEQUENCE 91 AA; 10082 MW; D0D6EAEBAE4242FF CRC64;

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Query Match 27.3%; Score 98.5; DB 11; Length 91;
Best Local Similarity 36.4%; Pred. No. 8.4e-05;
Matches 20; Conservative 10; Mismatches 24; Indels 1; Gaps 1;

OY 8 PCPCRFESHVARANKHLKILNTPNCALQIYARLKNRRQVCIDPKLKWIOEYL 62
DB 32 PCCEAYLSAVLPRAHKEY-FYTSSKCSNFAVEFVTRRNROYCANPKKRWQERYI 85

RESULT 5
Q90ZT0 PRELIMINARY: PRT: 363 AA.
AC Q90ZT0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Dystrophin variant Dp71 (Fragment).
GN DMD.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184125; PubMed=11287201;
RA Bolanos-Jimenez F., Borda A., Behra M., Strahle U., Sahel J.,
RA Rendon A.;
RT "Dystrophin and Dp71, two products of the DMD gene, show a different
RT pattern of expression during embryonic development in zebrafish.";
RL Mech. Dev. 102:239-241(2001).

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=FORESKIN;  
 RA Bartels J.H., Schueter C., Richter E., Noso N., Christophers E.,  
 Schroeder J.M.;  
 RT "Expression of a MCP-4 like novel CC-chemokine in human dermal  
 fibroblasts: molecular cloning and RT-PCR analysis";  
 RT Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 DL EMBL: Z77650; CAB0111.1; -.  
 DR HSSP; P51671; 1E0T.  
 DR InterPro: IPR000827; CC\_chemokine\_sm1.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PF00048; IL8; 1.  
 DR SMART; SM00199; SCY; 1.  
 DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
 FT NON\_TER  
 SQ SEQUENCE 79 AA; 8987 MW; 4FCF42983D46C352 CRC64;

Query Match 23.4%; Score 84.5; DB 4; Length 79;  
 Best Local Similarity 30.2%; Pred. No. 0.0041;  
 Matches 19; Conservative 15; Mismatches 24; Indels 5; Gaps 3;

OY 4 SLSPGCPRF-FESHVARANKHLK--ILNTPNCALQIVARLKNRQVCIDPKIKWIOE 60  
 Db 11 ALWPSGCTCFSS--KKISLQRLKXSVITTSRCPOKAVIFRRKLGEICADPREKKNVON 68  
 OY 61 YLE 63  
 Db 69 YMK 71

RESULT 10  
 OY1493 PRELIMINARY; PRT; 883 AA.  
 AC OY1493;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, last annotation update)  
 DE Dystrophin (Fragment).  
 GN DYSTROPHIN.  
 OS Torpedo californica (Pacific electric ray).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Squalae; Hypnosqualae; Pristigastera; Batoidae;  
 OC Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.  
 OX NCBI\_TaxID=7787;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92064638; PubMed=1720119;  
 RA Yeaman J.E., Lin H., Dyer S.M., Burden S.J.;  
 RT "Dystrophin is a component of the subsynaptic membrane";  
 RL J. Cell Biol. 115:1065-1076(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92291902; PubMed=1818109;  
 RA Ravin A.J., Dyer S.M., Yeaman J.E., Burden S.J.;  
 RT "Multiple dystrophin isoforms are associated with the postsynaptic  
 membrane of Torpedo electric organ";  
 RL J. Physiol. (Paris) 85:131-133(1991).  
 DR EMBL: M37645; AAC38002.1; -.  
 DR InterPro: IPR002017; Spectrin.  
 DR InterPro: IPR001202; WW\_Rsp5\_WWP.  
 DR InterPro: IPR000433; Znf\_ZZ.  
 DR Pfam: PF00435; spectrin; 2.  
 DR Pfam: PF00397; WW; 1.  
 DR Pfam: PF00569; ZZ; 1.  
 DR SMART; SM00150; SPEC; 2.  
 DR SMART; SM00456; WW; 1.  
 DR SMART; SM00291; Znf\_ZZ; 1.  
 DR PROSITE; PS01159; WW\_DOMAIN\_1; 1.  
 DR PROSITE; PS50020; WW\_DOMAIN\_2; 1.  
 DR PROSITE; PS01357; ZF\_ZZ\_1; UNKNOWN\_1.

FT NON\_TER 1 1  
 SQ SEQUENCE 883 AA; 101398 MW; F820BF58AB62B8C CRC64;

Query Match 23.4%; Score 84.5; DB 13; Length 883;  
 Best Local Similarity 33.9%; Pred. No. 0.048;  
 Matches 20; Conservative 7; Mismatches 27; Indels 5; Gaps 1;

OY 5 LSPGCPRFESHVARANKHLKILNTPNCALQIVARLKNRQVCIDPKIKWIOE 58  
 Db 322 LSPGCEAFDQINKKNDLIDLEINCLTSTYDLEQEHSLNVPICVCMCLNWL 380

RESULT 11  
 OYVAV9 PRELIMINARY; PRT; 134 AA.  
 AC OYVAV9;  
 DT 01-MAY-1999 (TREMblrel. 10, Created)  
 DT 01-MAY-1999 (TREMblrel. 10, last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, last annotation update)  
 DE VIL8 (CXC chemokine VIL8).  
 GN MDV003 OR MDV078.  
 OS Gallid herpesvirus 1,  
 OS Marek's disease herpesvirus (strain GA) (MDV), and  
 OS Marek's disease herpesvirus (strain Md5) (MDHV), Turkey herpesvirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.  
 OX NCBI\_TaxID=10386, 10388, 10389;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Gallid herpesvirus 1; STRAIN=RB1B;  
 RA Rasschaert D., Fragnet L.;  
 RT "Characterisation of the BamHI L fragment of the Marek's disease virus  
 RT RB1B strain (serotype 1).";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Marek's disease herpesvirus (strain GA) (MDHV);  
 RA Lin S.-F., Robinson D., Chen H.-C., Kung H.-D.;  
 RT "CXC chemokine encoded by Marek's Disease Virus (MDV).";  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Marek's disease herpesvirus (strain Md5) (MDV);  
 RX MEDLINE=20392152; PubMed=10933706;  
 RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;  
 RT "The genome of a very virulent Marek's disease virus.";  
 RL J. Virol. 74:7980-7988(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Marek's disease herpesvirus (strain Md5) (MDV);  
 RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF331499; AAL58097.1; -.  
 DR EMBL: AF065430; AAC77449.1; -.  
 DR EMBL: AF243438; AAG14290.1; -.  
 DR EMBL: AF243438; AAG14256.1; -.  
 DR HSSP; P10889; IMI2.  
 DR InterPro: IPR001089; CXC\_chemokine\_IL8.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PF00048; IL8; 1.  
 DR PRINTS; PR00437; SMALL\_CYTOKIN\_C.  
 DR SMART; SM00199; SCY; 1.  
 SQ SEQUENCE 134 AA; 14828 MW; C859GCD8868D25190 CRC64;

Query Match 22.9%; Score 82.5; DB 12; Length 134;  
 Best Local Similarity 27.5%; Pred. No. 0.013;  
 Matches 22; Conservative 14; Mismatches 17; Indels 27; Gaps 4;

OY 2 GVSLSYPCGPRFESHVARANKHLKILNTP-----NCALQIVARLKN 44  
 Db 22 GISL-----ESLAVDRKCKVKNPTGPIIADVPIPGICRRTETIFALK 71  
 OY 45 NNROVCTIDPKIKWIOEYLEK 64

RX MEDLINE=98167843; PubMed=9499411; SEQUENCE FROM N.R.

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RESULT 15
Q67634 PRELIMINARY; 3 PRT; 203 AA.
AC Q67634;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Eco Q protein (Fragment).
OS Marek's disease herpesvirus (strain GA) (MDHV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Marek's disease-like viruses.
OX NCBI_TaxID=10388;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GA;
RX MEDLINE=96074534; PubMed=7491783;
RA Peng Q., Zeng M., Bhuiyan Z.A., Ubukata E., Tanaka A., Nonoyama M.,
RA Shirazi Y.;
RT "Isolation and characterization of Marek's disease virus (MDV) cDNAs
RT mapping to the BamHI-I2, BamHI-Q2, and BamHI-L fragments of the MDV
RT genome from lymphoblastoid cells transformed and persistently infected
RT with MDV.";
RL Virology 213:590-599(1995).
DR EMBL; U34966; AAC54629.1; -.
DR HSSP; P10889; 1MI2.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR001089; CXC_chemokine_smll.
DR InterPro; IPR004827; TF_DZIP.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTKXC.
DR SMART; SM00338; BRLZ; 1.
DR SMART; SM00199; SCV; 1.
FT NON_TER 1
SQ SEQUENCE 203 AA; 23132 MW; DE42F2A1C1A71C88 CRC64;

Query Match 22.2%; Score 80; DB 12; Length 203;
Best Local Similarity 28.4%; Pred. No. 0.04;
Matches 19; Conservative 13; Mismatches 17; Indels 18; Gaps 3;

QY 15 ESHVARANVKHLKILNTP-----NC-ALQIVARLKNNNRQVCIDPKLKW 57
Db 95 ESLAVDKRCKVKVTRPTGLPIAVDVIPPGIHGRRTTEIIFALK-KNRKVCVDPEAPW 153
QY 58 IOEYLEK 64
Db 154 VQOFIKK 160

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